

Db 148 YRGIIPIVYQPCMKKGVRFTINGHDYFQLVLTINVAAGSIKAMDVKSKSPDMA 207
 QY 202 MSRRNGSMNQSNAYLINGSLSPRVTTTDETRVFODIVPVSMTFGQTFSSPVQF 255
 Db 208 MAHNGAQMHSLAYLTGGLSPRVTTTDDQTLVFPVNAVPGMRFGQTFASNIOF 261

RESULT 14 US-10-437-963-136422

/ Sequence 136422, Application US/10437963
 / Publication No. US20040123343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 136422
 / LENGTH: 250
 / TYPE: PRT
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_38002C.1.pep
 US-10-437-963-136422

Query Match 66.7%; Score 936.5; DB 4; Length 250;
 Best Local Similarity 68.8%; Pred. No. 9.8e-82;
 Matches 165; Conservative 35; Mismatches 33; Indels 7; Gaps 2;

QY 16 CFTITTAASPSGWTMAHATFYGGSDASGTMGACGYGNLYATGCTRTAALSTALFNDG 75
 Db 17 CIAATTAALSGT-----ATFYGGSDASGTMGACGYGNLYSTGYNTAALSSALFNDG 70
 QY 76 ASGQGCYKTIICDYKSDSRMCIGRSVTVATNFCPPNFALPNNNGMCNPLKHPDMAOP 135
 Db 71 AACGECYQITCD-QSNKSKCKAGTSTYTRATNLCPPDYKPSNDGCMCPRHFDMAOP 129
 QY 136 AWEKIGIYRGIVPVLFORVPCPKKGVRFPVNGRDYFELVLISNVGAAGSIQSVFIKGS 195
 Db 130 AWEQIGVYRGIVPVLFORVSCTRKKGVRFTINGNSYFELVLITNVGPGSISVQIKGT 189
 QY 196 KTGMMAMSRNNGSMNQSNAYLINGSLSPRVTTTDETRVFODIVPVSMTFGQTFSSPVQF 255
 Db 190 KTGVMVTSRRNGAMQANNYLNNOAISFSVSTAGKTLVFEDEVAPSNMQFGQTFISGVQF 249

RESULT 15

US-10-437-963-133869
 / Sequence 133869, Application US/10437963
 / Publication No. US20040123343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14

/ NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 133869
 / LENGTH: 617
 / TYPE: PRT
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_35699C.1.pep
 US-10-437-963-133869

Query Match 66.2%; Score 928.5; DB 4; Length 617;
 Best Local Similarity 64.2%; Pred. No. 1.7e-80;
 Matches 165; Conservative 33; Mismatches 54; Indels 5; Gaps 2;

QY 4 IMLVGSLIGLCCFTITTY---AFSPSGWTMAHATFYGGSDASGTMGACGYGNLYATG 59
 Db 10 VLLAVASASTAANATTTPTNPVAAPQWQKHAHTFYGDADASGTMGACGYGNLYSQG 69
 QY 60 YGTRTAALSTALFNDGASGQCYKTIICDYKSDSRMCIGRSVTVATNFCPPNFALPNNN 119
 Db 70 YGTRNAALSTALFNDGASGQCYKTIACDKRAPOCKEKGVTITRATNFCPPNNMLPSDN 129
 QY 120 GGMCPPLKHPDMAOPAMEKIGIYRGIVPVLFORVPCPKKGVRFPVNGRDYFELVLIS 179
 Db 130 GGMCPPRPHFDMAOPAMEKIGVSAGLIPVYQRPVCKKGLFTINGHDYFQLVLVT 189
 QY 180 NVGAGASIQSVFIKSKTG-NMAAMSRNNGSMNQSNAYLINGSLSPRVTTTDETRVFODI 238
 Db 190 NVAAAGSIKSMVMSNTADMMPMARNNGAQMHSLAYLTGGLSPRVTTTDDQTLVFTNV 249
 QY 239 VPVSMTFGQTFSSPVQF 255
 Db 250 VPPGKWFQGTFSKIQF 266

Search completed: January 10, 2006, 12:40:53
 Job time : 63 secs


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/ Sequence 7, Application US/10197294A
/ Publication No. US20030104546A1
/ GENERAL INFORMATION:
/ APPLICANT: Swanson, Barbara A.
/ APPLICANT: Ward, Michael
/ APPLICANT: Penttila, Merja
/ APPLICANT: Pere, Jaakko
/ APPLICANT: Saloelmo, Markku
/ TITLE OF INVENTION: Microbial Swollenin Protein, DNA
/ TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
/ FILE OF INVENTION: Such Swollenins
/ FILE REFERENCE: GC378-2-D1
/ CURRENT APPLICATION NUMBER: US/10/197,294A
/ CURRENT FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: US 09/112,498
/ PRIOR FILING DATE: 1998-07-09
/ PRIOR APPLICATION NUMBER: US 08/893,766
/ PRIOR FILING DATE: 1997-07-11
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 234
/ TYPE: PRT
/ ORGANISM: Plant/eukaryotic
US-10-197-294A-7
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Query Match      78.2%; Score 1097.5; DB 4; Length 234;
Best Local Similarity 82.8%; Pred. No. 2.8e-97;
Matches 193; Conservative 21; Mismatches 18; Indels 1; Gaps 1;
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```
QY      24 FSPSGTNAHATFYGGSDASGTMGACGYGNLYATGYGRTALSTALFNDGASCGQCYK 83
      1 FASGAPAAHATFYGGSDASGTMGACGYGNLYQTYGRTALSTALFNDGASCGQCYK 60
QY      84 IICDYSDSRWCIKGSVTVTATNFCPPPALPNNNGMCNPLKHFMAQAPAMEKIGIY 143
      61 IICDYKTDPRWCKGASVITATNFCPPPALPNNNGMCNPLKHFMAQAPAMEKIGIY 120
DB      144 RGIIVFVLFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSIQSVFIKSK-TGMMAM 202
      121 RGIIVFVLFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSIQSVFIKSK-SMTMTPM 180
QY      203 SRNWSNWSNAYLNGQSLSFRVTTTDTGETRVFQDIYVSVTFQTFSSPVQF 255
      181 SRNWSNWSNAYLNGQSLSFRVTTTDTGETRVFQDIYVSVTFQTFSSPVQF 233
DB
```

```
RESULT 6
US-10-425-115-355473
/ Sequence 355473, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 355473
/ LENGTH: 262
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_87357C.1.pcp
US-10-425-115-355473
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Query Match      74.3%; Score 1043; DB 4; Length 262;
Best Local Similarity 75.0%; Pred. No. 5.7e-92;
Matches 186; Conservative 24; Mismatches 38; Indels 0; Gaps 0;
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```
QY      8 LSLIGLCCFTITTYTAFSPSGTNAHATFYGGSDASGTMGACGYGNLYATGYGRTAL 67
      14 LALLLAACILMKREACFSASGLNKAFATFYGGSDASGTMGACGYGNLYSTGYDTTAL 73
QY      68 STALFNDGASCGQCYKIICDYSDSRWCIKGSVTVTATNFCPPPALPNNNGMCNPL 127
      74 STALFNDGASCGQCYKRISCDYQADPRFCIRGTSVITATNLCPPPALPNDGMCNPPR 133
DB      128 KHFMAQAPAMEKIGIYRGIVLVFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSI 187
      134 QHFMAQAPAMEKIGIYRGIVLVFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSI 193
QY      188 QSVFIKSKRTGMMASRNWGSNAYLNGQSLSFRVTTTDTGETRVFQDIYVSVTFQ 247
      194 QASIKSKRTGMMASRNWGSNAYLNGQSLSFQVTSISDQITKTFPDVAPASWGFQ 253
DB      248 TFSSPVQF 255
      254 TFATSQQF 261
```

```
RESULT 7
US-10-425-114-52645
/ Sequence 52645, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven B.
/ APPLICANT: Tabaska, Jack B.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 52645
/ LENGTH: 273
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3067-046-B8_F1.1.pcp
US-10-425-114-52645
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Query Match      74.3%; Score 1043; DB 4; Length 273;
Best Local Similarity 75.0%; Pred. No. 6e-92;
Matches 186; Conservative 24; Mismatches 38; Indels 0; Gaps 0;
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```
QY      8 LSLIGLCCFTITTYTAFSPSGTNAHATFYGGSDASGTMGACGYGNLYATGYGRTAL 67
      25 LALLLAACILMKREACFSASGLNKAFATFYGGSDASGTMGACGYGNLYSTGYDTTAL 84
DB      68 STALFNDGASCGQCYKIICDYSDSRWCIKGSVTVTATNFCPPPALPNNNGMCNPL 127
      85 STALFNDGASCGQCYKRISCDYQADPRFCIRGTSVITATNLCPPPALPNDGMCNPPR 144
QY      128 KHFMAQAPAMEKIGIYRGIVLVFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSI 187
      145 QHFMAQAPAMEKIGIYRGIVLVFQRYVPCCKHGGVRSVNGRDYFELVLISNVGAGSI 204
QY      188 QSVFIKSKRTGMMASRNWGSNAYLNGQSLSFRVTTTDTGETRVFQDIYVSVTFQ 247
      205 QASIKSKRTGMMASRNWGSNAYLNGQSLSFQVTSISDQITKTFPDVAPASWGFQ 264
DB      248 TFSSPVQF 255
      265 TFATSQQF 272
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RESULT 8


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; Sequence 51485, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51485
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700944591_FLI.pep
US-10-425-114-51485

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Query Match          99.7%; Score 1399; DB 4; Length 263;
Best Local Similarity 99.6%; Pred. No. 2,9e-126;
Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MGKIMLVLSLIGLCFFITTTTAAFPSPSGWTNAHATYGGSDASGTMGACGYNLYATGY 60
DB 9 MGKIMLVLSLIGLCFFITTTTAAFPSPSGWTNAHATYGGSDASGTMGACGYNLYATGY 68
QY 61 GRTTALSTALFNDGASCGQCYKIIDYXSDSRWCIGKRSVYVTAATNFCPPNFALPNNNG 120
DB 69 GRTTALSTALFNDGASCGQCYKIIDYXSDSRWCIGKRSVYVTAATNFCPPNFALPNNNG 128
QY 121 GNCNPLKHPDMAQPAWEKIGIYRGIVPVLFORVCKKHGVRFSVNGRDYFELVLSN 180
DB 129 GNCNPLKHPDMAQPAWEKIGIYRGIVPVLFORVCKKHGVRFSVNGRDYFELVLSN 188
QY 181 VEGAGSIGVFYKSGTKGMMASRNWGSNWSNAYLNGQSLSFRTVTTDGETRFQDIYV 240
DB 189 VEGAGSIGVFYKSGTKGMMASRNWGSNWSNAYLNGQSLSFRTVTTDGETRFQDIYV 248
QY 241 VSWTFGOTFSSPVQF 255
DB 249 ASWTFGOTFSSPVQF 263

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RESULT 3
US-10-730-866-23
; Sequence 23, Application US/10730866
; Publication No. US20040132617A1
; GENERAL INFORMATION:
; APPLICANT: Cogrove, Daniel J
; TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
; FILE REFERENCE: 11940E183
; CURRENT APPLICATION NUMBER: US/10/730,866
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/071,252C
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/045,445
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-10-730-866-23

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```

Query Match          78.7%; Score 1103.5; DB 4; Length 258;
Best Local Similarity 81.2%; Pred. No. 8.3e-98;

```

```

Matches 195; Conservative 22; Mismatches 22; Indels 1; Gaps 1;
QY 17 FTITTAAPSPSGWTNAHATFYGGSDASGTMGACGYNLYATGYGRTTALSTALFNDGA 76
DB 18 FFLPVNATFASGMAPAHATFYGESDASGTMGACGYNLYOYGYGRTTALSTALFNDGA 77
QY 77 SCGQCYKIIDYKDSRWICIKRSVYVTAATNFCPPNFALPNNNGCNPPLKHPDMAQPA 136
DB 78 SCGQCYKIIDYKDSRWICIKRSVYVTAATNFCPPNFALPNNNGCNPPLKHPDMAQPA 137
QY 137 WEKIGIYRGIVPVLFORVCKKHGVRFSVNGRDYFELVLSNNGAGSISQVFYKSGK 196
DB 138 WOKIIGYGGIIPVLYORVPCCKRGVRFTVNGRDYFELVLTNNVGAGDIDSVYKSGK 197
QY 197 -TGMMASRNWGSNWSNAYLNGQSLSFRTVTTDGETRFQDIYVSWTFGOTFSSPVQF 255
DB 198 SSWTFGOTFSSPVQF 257

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RESULT 4
US-09-112-498A-6
; Sequence 6, Application US/09112498A
; Publication No. US20020086350A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SMOLLENIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SMOLLENINS AND METHOD OF PRODUCING SUCH
; TITLE OF INVENTION: SKOLLENINS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-112-498A-6

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Query Match          78.2%; Score 1097.5; DB 3; Length 234;
Best Local Similarity 82.8%; Pred. No. 2.8e-97;
Matches 193; Conservative 21; Mismatches 18; Indels 1; Gaps 1;
QY 24 FPPSGWTNAHATFYGGSDASGTMGACGYNLYATGYGRTTALSTALFNDGASCGQCYK 83
DB 1 FTAAGMAPAHATFYGESDASGTMGACGYNLYOYGYGRTTALSTALFNDGASCGQCYK 60
QY 84 IICDYKDSRWICIKRSVYVTAATNFCPPNFALPNNNGCNPPLKHPDMAQPAWEKIGIY 143
DB 61 IICDYKDSRWICIKRSVYVTAATNFCPPNFALPNNNGCNPPLKHPDMAQPAWEKIGIY 120
QY 144 RGGIIPVLYORVPCCKKHGVRFSVNGRDYFELVLSNNGAGSISQVFYKSGK-TGMMAM 202
DB 121 RGGIIPVLYORVPCCKKHGVRFSVNGRDYFELVLTNNVGAGDIDSVYKSGKSNWTM 180
QY 203 SRWGSNWSNAYLNGQSLSFRTVTTDGETRFQDIYVSWTFGOTFSSPVQF 255
DB 181 SRWGSNWSNAYLNGQSLSFRTVTTDGETRFQDIYVSWTFGOTFSSPVQF 233

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RESULT 5
US-10-197-294A-7

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 10, 2006, 12:32:44 ; Search time 62 Seconds
(without alignments)
1718.492 Million cell updates/sec

Title: US-10-660-499a-2
Perfect score: 1403
Sequence: 1 MGKIMLVGSLIGLCCFTIT.....QDIVPVSWTGGTFSSPVQF 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1399	99.7	255	4 US-10-424-599-191193	Sequence 191193,
2	1399	99.7	253	4 US-10-425-114-51485	Sequence 51485, A
3	1103.5	78.7	258	4 US-10-730-866-23	Sequence 23, Appl
4	1097.5	78.2	234	3 US-09-112-498A-6	Sequence 6, Appl1
5	1097.5	78.2	234	4 US-10-197-294A-7	Sequence 7, Appl1
6	1043	74.3	252	4 US-10-425-115-355473	Sequence 355473,
7	1043	74.3	273	4 US-10-425-114-63947	Sequence 52645, A
8	1043	74.3	273	4 US-10-425-114-63947	Sequence 63947, A
9	1042	74.3	284	4 US-10-425-114-65439	Sequence 65439, A
10	1039	74.1	261	4 US-10-437-963-203012	Sequence 203012,
11	1039	74.1	263	4 US-10-730-866-36	Sequence 36, Appl
12	987	70.3	253	4 US-10-437-963-178982	Sequence 178982,
13	971.5	69.2	355	4 US-10-437-963-132056	Sequence 132056,
14	968.5	66.7	250	4 US-10-437-963-136422	Sequence 136422,
15	928.5	66.2	253	4 US-10-437-963-133869	Sequence 133869,
16	923	65.8	223	3 US-09-112-498A-3	Sequence 3, Appl1
17	923	65.8	223	4 US-10-197-294A-4	Sequence 4, Appl1
18	920	65.6	262	4 US-10-437-963-197264	Sequence 197264,
19	920	65.6	280	4 US-10-437-963-196205	Sequence 196205,
20	919	65.5	228	4 US-10-767-701-46559	Sequence 46559, A
21	914.5	65.2	278	4 US-10-437-963-197265	Sequence 197265,
22	913	65.1	264	4 US-10-425-114-49606	Sequence 49606, A
23	911.5	65.0	254	4 US-10-424-599-248554	Sequence 248554,
24	909	64.8	250	4 US-10-424-599-219709	Sequence 219709,
25	905	64.5	250	4 US-10-424-599-238586	Sequence 238586,
26	901.5	64.3	222	4 US-10-197-294A-5	Sequence 5, Appl1
27	901	64.2	251	4 US-10-437-963-141025	Sequence 141025,

28	900.5	64.2	731	4 US-10-437-963-133876	Sequence 133876,
29	898	63.8	249	5 US-10-739-920-6630	Sequence 6630, Ap
30	894.5	63.0	251	4 US-10-437-963-204527	Sequence 204527,
31	892.5	63.6	277	4 US-10-425-114-44234	Sequence 44234, A
32	892.5	63.6	288	4 US-10-424-599-246765	Sequence 246765,
33	890.5	63.5	237	3 US-09-112-498A-7	Sequence 7, Appl1
34	890.5	63.5	254	4 US-10-730-866-37	Sequence 37, Appl
35	889	63.4	227	3 US-09-112-498A-5	Sequence 5, Appl1
36	886.5	63.2	250	4 US-10-730-866-22	Sequence 22, Appl
37	885	63.1	249	4 US-10-425-114-48667	Sequence 48667, A
38	884.5	63.0	228	3 US-09-896-301-2	Sequence 2, Appl1
39	883.5	63.0	290	4 US-10-424-599-246787	Sequence 246787,
40	881	62.8	245	4 US-10-425-115-278533	Sequence 278533,
41	879	62.7	227	3 US-09-896-301-7	Sequence 7, Appl1
42	879	62.7	236	4 US-10-197-294A-8	Sequence 8, Appl1
43	878	62.6	259	4 US-10-424-599-269181	Sequence 269181,
44	873	62.2	245	4 US-10-425-115-278522	Sequence 278522,
45	873	62.2	254	4 US-10-437-963-185711	Sequence 185711,

ALIGNMENTS

RESULT 1
US-10-424-599-191193
; Sequence 191193, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191193
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14667C.1.pep
US-10-424-599-191193

Query Match 99.7%; Score 1399; DB 4; Length 255;
Best Local Similarity 99.6%; Pred: No. 2, 8e-126;
Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKIMLVGSLIGLCCFTITTYAFSPSGWTNHAATFYGSDASGTWGACGYGNLYATGY 60
1 MGKIMLVGSLIGLCCFTITTYAFSPSGWTNHAATFYGSDASGTWGACGYGNLYATGY 60
Db 1 MGKIMLVGSLIGLCCFTITTYAFSPSGWTNHAATFYGSDASGTWGACGYGNLYATGY 60
QY 61 GRTTALSTALFNDGASGCGCTKIITDYSDSWCTKGSVYVTATNFCPPNPALENNNG 120
61 GRTTALSTALFNDGASGCGCTKIITDYSDSWCTKGSVYVTATNFCPPNPALENNNG 120
Db 61 GRTTALSTALFNDGASGCGCTKIITDYSDSWCTKGSVYVTATNFCPPNPALENNNG 120
QY 121 GWCNPLKHPDMAQPMWEKIGIYRGSIYVPLRQVPCCKHGGVRSFVNRDPELVLI 180
121 GWCNPLKHPDMAQPMWEKIGIYRGSIYVPLRQVPCCKHGGVRSFVNRDPELVLI 180
Db 121 GWCNPLKHPDMAQPMWEKIGIYRGSIYVPLRQVPCCKHGGVRSFVNRDPELVLI 180
QY 181 VGGAGSIQSVFTKSGKTYGMAMSRMGSNMOSNAYLNGOSLSFRVTTTGTETRVFODI 240
181 VGGAGSIQSVFTKSGKTYGMAMSRMGSNMOSNAYLNGOSLSFRVTTTGTETRVFODI 240
Db 181 VGGAGSIQSVFTKSGKTYGMAMSRMGSNMOSNAYLNGOSLSFRVTTTGTETRVFODI 240
QY 241 VSWTFQGTSSPVQF 255
241 VSWTFQGTSSPVQF 255
Db 241 ASWTFQGTSSPVQF 255
241 ASWTFQGTSSPVQF 255

RESULT 2
US-10-425-114-51485

XX Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX Claim 1; SEQ ID NO 7077; 2576bp; English.

XX The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.

XX SQ Sequence 634 BP; 177 A; 119 C; 149 G; 189 T; 0 U; 0 Other;

Query Match 29.7%; Score 323.2; DB 10; Length 634;

Best Local Similarity 73.3%; Pred. No. 4.3e-63;

Matches 428; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 40 CAAAGAAAAAATGGGCAAAATCATGCTTTGGGTAGCCCTCATGTATATGCTG 99
DB 44 CTAAGAAAAATGGCTAAATGCGATCTAGCACTGGGATTCATTAATGGTTTGCAAC 103
QY 100 TTGCAATCATCTACCTATGCTCTGACC---TTCTGATGSAACAAGGCCATGCACT 156
DB 104 CTTTCTTAAGTGCAAAATGGTTTTCAGAGATTTGAGTGTCAAGTGTCTCATGCCACA 163
QY 157 TTTTATGGGGGTAGTATGCTTCAGAACTATGGGGAGCTTGTGGTATGGGAATCTG 216
DB 164 TTTTATGTGTAGAGCTGATGCTTCGCGACATAGGGGGGTGCTGTGATATGGAACTTG 223
QY 217 TATGCAACTGGGTATGGAATCTAGACTGCACTTAAAGCACTGCTTATTTATGATGA 276
DB 224 TATTCACAAGGGTATGGAACAAGACAGCTGCATTTAGCACTGCATTTTCAATGATGA 283
QY 277 GCTTCCTGTGTGCTAGTCTCAAAATTAATGATTAACAATGACACTAGATGCTG 336
DB 284 GGAATCTGTGCTCAATGCTACAGATCATATGATTAAGGCAACCCGCAATGCTG 343
QY 337 ATCAAGAGAGATCTGTACCGTAACTGCCAACAATTTGCTCCCAATTTGCCCTT 396
DB 344 AAGAGAGGAGATCTGTACATTAACAGCTACAAATTTTGCACCAATTAATCAATCTT 403
QY 397 CTTAACAACAATGAGGCTGTGCAACCACTCAAGCATTTTGAATATGCCCCAACCC 456
DB 404 CTTAGTAACAATGAGGCTGTGTAACCTCTCGTCCCATTTTGAATATGCTCAACT 463
QY 457 GCTTGGGAAAAAGATTGTATTTACAGAGAGGATCGTCCCGCTATTTCAAGGTT 516
DB 464 GCTTGGGAAAAAGATTGTATTTACAAAGAGGCAATGTTCTGTGCTTACAAAGGTT 523
QY 517 CCATGCAAAAAAGCATGAGGGGTAGGTTCACTGATGATGAGGAGACTACTTTGAGCTA 576
DB 524 CTTTGCAAGAAACAATGAGTTAGATTCATCAATGGAAGGACTATTTGAACCTA 583
QY 577 GTATATGATCAGCAATGTGGGGGTGTGATTCATTCATCAATCAATGAT 620
DB 584 GTCTTGTAGCAATGTAGCAGGGGCAAGATCTGTCAATCTGT 627

Search completed: January 11, 2006, 10:42:26
Job time : 701 secs

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 28800; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX
 SQ Sequence 1053 BP; 180 A; 336 C; 315 G; 222 T; 0 U; 0 Other;
 XX
 Query Match 30.7%; Score 334.8; DB 13; Length 1053;
 Best Local Similarity 67.5%; Pred. No. 1.2e-65;
 Matches 471; Conservative 0; Mismatches 227; Indels 0; Gaps 0;
 QY 120 CTTCTCACTTGTGATGACCAACGCCCATGTCATTGTTGAGGAGTATGCTTC 179
 DB 163 CTTCTCGGCGTCCGGGTAAACAAAGGCGTTCGACCTTCATGCGGTGACGACGCTTC 222
 QY 180 AGGAACATATGGGGGAGACTGTGGGTATGGGAATCTGTATGCAACTGGGTATGGAATTAG 239
 DB 223 AGGAACATATGGGTGGCTGTGGGTATCGGCAACTGTACTCGACGGGGTATCGGACGGA 282
 QY 240 AACTGACGCTTAAAGCACTGCTTATTTAATGATGAGGCTTCGTTGATGAGCTCA 299
 DB 283 CACGGCGGGCTAGACAGCGGCGCTTCAACGACGCGCGCTGTGGCGGAGTGTACCG 342

QY 300 AATTATATGATTTAACAATCAGACTCTAGATGGTGACATCAAGGAAGATCTGAACCGT 359
 DB 343 GAATCCCTGTGACATCCAGCGGAGACCGCGGTTCTGATCGGGACGTCGGTACAT 402
 QY 360 AATCGCAACAATTTTGGCCCTCCCAATTTGGCCCTTCTTAACAACAATGAGGCTGGT 419
 DB 403 CACCGCCACCAACTGTGGCTCTCCCACTAGCGGCTGCCAAGCAAGACGCGGCTGGT 462
 QY 420 CAACCCACCACTGAAGATTGATATGGCCCAACCGCTGGGAAAAGATTGATTTA 479
 DB 463 CAACCCGCGCGGACGACTTTCAGATGGCCGAGCGGCTGGCTCAAGATCGGCATCTA 522
 QY 480 CAGAGAGAGATATGTCCTCCCTGCTATTTGAAAGGTTCCATGCAAAAAGATGAGGGGT 539
 DB 523 CCGCGGGGATGTGTGCTCCCTCAACTACCAAGGGTGGCGGTGTGAAGAAAGCGGGGT 582
 QY 540 TAGTTCAAGTGAATGGAGGAGTACTTGTGACTAGTATTTATGATCAGCAATGGGGGG 599
 DB 583 GAGGTTCAGATCAACGGGGGCACTACTTCCAGCTGTGCTCATCTTCAACGTGGGCGG 642
 QY 600 TGCTGATCCATCCATCAAGTGTTCATTAAAGGCTCAAAAATGATGATGGCAATGTC 659
 DB 643 CTGCGGGTCCATCCAGTCGGCGTCCATCAAGGGGTGGCGCACGGGTGATGGCATGTC 702
 QY 660 AAGAAATGGGGGTTCTTAATTTGGCAATCCCATGGCTATTGAATGTCATCTTGTCTT 719
 DB 703 CCGAACTGGGGGGGTCAACTGAGGAGTCCAAAGGCTCAATATGGCCAGAGCCCTGTCT 762
 QY 720 CAGGTCACCAACCACTGATGAGAGACAGAGTTTCCAAAGATATTGTTCCAGTAAGTTG 779
 DB 763 CCAAGTCAACGACGACGAGCGGCCAGACCAAAACCTTCCCGAAGTGGCGGCCAGCTG 822
 QY 780 GACATTCGGCCAAACTTCTCTAGCCCAAGTTCAGTTCT 817
 DB 823 GGGGTTGCGTCAAGACGTTTGCACCTCGACGAGTTCT 860
 XX
 RESULT 15
 ADKS59694
 ID ADKS59694 standard; DNA; 634 BP.
 XX
 AC ADKS59694;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Plant DNA sequence which confers altered metabolic characteristic #7077.
 XX
 KW altered metabolic characteristic; plant; acid metabolism;
 KW alcohol metabolism; fatty acid metabolism;
 KW branched fatty acid metabolism; alkaloid metabolism;
 KW amino acid metabolism; ester metabolism; glyceride metabolism;
 KW phenolic metabolism; carbohydrate metabolism; steroid metabolism;
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003020936-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027884.
 XX
 PR 31-AUG-2001; 2001US-0316471P.
 XX
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Meglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
 PI Oriedo UVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
 DR WPI; 2003-313091/30.

```

Db      565 TCMAATGATGAGGAGGAGGAGGTTCTTAATATCTGATCATCAAGATCAAGACTG 624
Qy      645 ATGAGATGCAATGTCAGAAATTTGGGCTTCTAATTTGGCAATCCAAATGCTTGAATG 704
Db      625 TTGGTTAGCCATGCTCTGTAATTTGGGAGCTAATTTGGCAATGCAATGCTTAATCTAGATG 684
Qy      705 TCAATCTTTGT 715
Db      685 TCMACTCTCT 695

RESULT 13
ADX34192
ID      ADX34192 standard; cDNA; 1029 BP.
XX
XX      ADX34192;
XX
XX      21-APR-2005 (first entry)
XX
DE      Plant full length insert polynucleotide seqid 17012.
XX
XX      plant protectant; plant growth regulant; gene therapy; plant;
XX      recombinant DNA construct; physical array; plant breeding marker;
XX      cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX      extreme osmotic condition; pathogen tolerance; pest tolerance;
XX      growth rate; cell cycle pathway; disease resistance;
XX      galactomannan production; lignin production; plant growth regulator;
XX      yield; plant growth; plant development; seed oil; protein yield;
XX      protein content; gene; ss.
XX
OS      Unidentified.
XX
XX      US2004034888-A1.
XX
XX      19-FEB-2004.
XX
XX      28-APR-2003; 2003US-00425114.
XX
XX      06-MAY-1999; 99US-00304517.
XX      05-NOV-2001; 2001US-00985678.
XX
XX      (LIU/) LIU J.
XX      (ZHOU/) ZHOU Y.
XX      (KOVA/) KOVALIC D K.
XX      (SCRE/) SCREEN S E.
XX      (TABAS/) TABASKA J E.
XX      (CAOY/) CAO Y.
XX
PI      Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX      MPI; 2004-180133/17.
XX
XX      New recombinant DNA construct, useful for improving plant tolerance to
XX      cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX      pests, for conferring increased resistance to plant disease, or for
XX      improving yield.
XX
XX      Claim 1; SEQ ID NO 17012; 15pp; English.
XX
XX      The invention describes a recombinant DNA construct comprising a
XX      polynucleotide consisting of a sequence encoding an amino acid sequence
XX      available in electronic form from the US patent office at
XX      ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX      of the invention are also useful in physical arrays of molecules and as
XX      plant breeding markers. The recombinant DNA construct is useful for
XX      improving plant tolerance to cold, heat, drought, herbicides, extreme
XX      osmotic conditions, pathogens or pests, for manipulating growth rate in
XX      plant cells by modification of the cell cycle pathway, for conferring
XX      increased resistance to plant disease, for producing galactomannan,
XX      lignin or plant growth regulators, for increasing the rate of homologous
XX      recombination in plants, for improving yield by modification of
XX      photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

```

CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

SQ Sequence 1029 BP; 182 A; 330 C; 304 G; 213 T; 0 U; 0 Other;

Query Match 30.7%; Score 334.8; DB 13; Length 1029;
 Best Local Similarity 67.5%; Pred. No. 1.2e-65;
 Matches 471; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

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Qy      120 CTTCTCACCTTGTGATGAGCAACGCCATCCACTTTTATGAGGGATGATGATGCTTC 179
Db      146 CTTCTCGGCGTCGGGCTTAACAGGCGTTCCGACCTTCTATGCGGATGAGCACTTC 205
Qy      180 AGGAATATGAGGGGAGCTTGTGGGTATGGGAATCTGTATGCAACTGGGTATGGAATCTG 239
Db      206 AGGAACGATGGGTGGGGCTGTGGGTACGGCAACTGTATCTGACCGGGATGCGCACGGA 265
Qy      240 AACTGAGCTTAAAGACTGACCTTATTTATATGATGAGGCTTCTGTGATCAAGTAA 299
Db      266 CACGGGCGCTGAGAGCAGCGCGCTTTCAACAGCGCGCTGTGTGCGGCACTGCTACCG 325
Qy      300 AATTATATGTATTAACAATCAGACTGTATGATGTGATCAAAAGAAATCTGTAACTG 359
Db      326 GATCTCTGCGACTACCAAGCGGACCCGGGTTCTGTATCTCGGCGACCTCGGTGACAT 385
Qy      360 AACTGCAACAACCTTGGCCCTTCCCAATTTGCCCTTCTTAACAACAATGAGAGCTGTG 419
Db      386 CACCGCAACAACCTGTGCTTCCCAATCTACGCGCTGCCAACAAGACGAGCGGCTGTG 445
Qy      420 CAACCCAGCACTCAAGCACTTTTGAATGTGGCCCAACCGCTGGGAAAGATGTGATTTA 479
Db      446 CAACCCGCGCGGCAAGCACTTGAACATGGCCAGCGCGCTGTGCTTAAGATCGGCATCTA 505
Qy      480 CAGAGAGGGAATGTCCTCCGCTATTTCAAAAGGTTTCCATGCAAAAGCAATGAGAGGAT 539
Db      506 CGCGGCGGCACTGTGTCCGCTCAATCAAAAGGTTCCGTGTGTGAAGAAAGCGGGGT 565
Qy      540 TAGGTTCAATGTGAATGAGAGGAGCTACTTTGAGCTAGTATGATCAACAATGTGGGG 599
Db      566 GAGGTTCAACATCAACAGGCGGAGCACTTCACTGAGCTGTCTCATCTCAACCTGTGG 625
Qy      600 TGTGATTCATTCATCAGTGTTCATTAAGGCTCAAAAATCTGATGATGAGCAATGTC 659
Db      626 CTGCGGCTCATTCAGTCTGCGCTTCATCAAGGGGTGCGGACCGGTGATGCAATGTC 685
Qy      660 AAGAAATGGGGTTCTAATTTGGCAATCCATGCGTATTTGAATGTCAATCTTTGCTT 719
Db      686 CCGGAATGGGGGTCAACTGGGAGTCCAAACGGTACCTCAATGGCCAGAGCTGTCT 745
Qy      720 CAGGTCACCAACCATGATGAGAGAGCAAGATTTTCCAAAGATATTTGCTCAATGTT 779
Db      746 CCAAGTCAACAGAGAGAGAGGCGGCAACAACTTTCCCGAGCTGCGCCGCGAGCTG 805
Qy      780 GACATTCGCGCAAACTTTCTTATGCCCCAGTTCAGTTCT 817
Db      806 GGGGTTGGTCAAGACGTTTGCAGCTTCGAGAGCTTCT 843

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RESULT 14
ADX54060
ID      ADX54060 standard; cDNA; 1053 BP.
XX
XX      ADX54060;
XX
XX      21-APR-2005 (first entry)
XX
DE      Plant full length insert polynucleotide seqid 28800.
XX
XX      plant protectant; plant growth regulant; gene therapy; plant;
XX      recombinant DNA construct; physical array; plant breeding marker;
XX
KW

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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145226P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154039P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.

PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157153P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160788P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.8%; Score 335; DB 3; Length 695;
Best Local Similarity 72.8%; Pred. No. 9, 6e-66;
Matches 445; Conservative 0; Mismatches 165; Indels 1; Gaps 1;

QY 106 ATCACTACCTAATCCCTTCACCTTCGATGAGCAAGCCCATCTTTATAGG 165
DB 85 ATTGCTGTGATCGCTTAAGCTTCGTGTTAAGCCACGCTACATTCATGGA 144
QY 166 GGTAGTGAATGCTTCAGAACTATGGGG-GGAGCTTGGGTATGGAAATCTGATGCAC 224
DB 145 GGAATGACCGCTTCGTGAACAATGGGGTGAAGCTTGGGTACGAGATCTTACCGGC 204
QY 225 TGGGTATGGAATAGAACTGCACTGCACTTTAAGCACTGCTTATTTAATGATGAGCTTCTG 284
DB 205 GGGGTACGGGACAATACGCGCAAGCGTTAAGCACGCGCTGTTCACAGCGAGACTTCTTG 264
QY 285 TGGTCACTGCTCAAAATATATATGATATCAAAATCAAGCTCAAGTGTGATCAAAAG 344
DB 265 CGAGAAATGCTAATGAGATTAACGTGATCAACGCGGAGCTCAAGTGTGCTTGAAGG 324
QY 345 AAGATCTGTAAACCGTAACCTGCAACAATTTTGCCCTCCCAATTTGCGCCCTTCTAACAA 404
DB 325 AGCTTCTGTGTTATTTACAGCCCACTAATTTTGCCCAACAATTTGCTTTGCTTAACAA 384
QY 405 CAATGAGAGCTGTGTGCAACCCCACTCAAGCAATTTGATATGATGAGCCCAACCGCTTGGA 464
DB 385 CAACGGTGGTTGTGTGAATCCGCGCTTAAACATTTTGACATGGCAACACCGCTTGGA 444
QY 465 AAAGATTGTATTTTACAGAGAGGATGCTCCCGGCTATTTTCAAAAGGTTCCATGCCA 524
DB 445 AAAGATCGAAATTTTACAGAGAGGATGCTCCCGCTTTCAAAGATGAGCTGTTA 504
QY 525 AAAGCATGAGGGGTTAGGTTAGTGTGATGAGGAGGACTACTTTGAGCTAGTATTTGAT 584
DB 505 CAAGAAAGAGAGGTTAGTATTCAGATTTAAACGGAAGAGACTTGTGAGCTAGTGAACAT 564
QY 585 CAGCAATGTGGGGGTGTGTGATTCATTCATGATGTTCAATTAAAGCTCAAAAACCTGG 644
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Best Local Similarity 67.6%; Pred. No. 5,1e-66;
Matches 472; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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QY 120 CTTCTCACTTCTGATGAGCAACGCCCATTCCTTTTATGGGGGTATGATGCTTC 179
    |||
DB 140 CTTCTCGGCTCTCGGGCTTAAACAAGGCTTCCGACCTTCTATGGGGTACCACTTC 199
    |||
QY 180 AGGAACATATGGGGGAGCTTGTGGGTATGGGAATCTGTATGACAACTGGGTATGAACTAG 239
    |||
DB 200 AGAAGCATATGGGTGGGGCTTGTGGGTATGGGAATCTGTATGACAACTGGGTATGAACTAG 259
    |||
QY 240 AACTGAGCTTTTAAAGCACTGCTTATTTAAATGATGAGCTTCTGTGTGATGCTAACAA 299
    |||
DB 260 CAGGGGGGGCTGAGAGCAGGCGCTCTTCAACGACGGGCTCGTGGGGGAGTGTACCG 319
    |||
QY 300 AATTATATGTGATTAACAATCACTTAATGATGTGTATCAAAAGAAATCTGTAACTGT 359
    |||
DB 320 GATCTCTGTGACTACACAGGCGGACCCGCGTCTGTGATCGGGCACTGTGGTGAACAT 379
    |||
QY 360 AACTGCAAACTTTTGGCCCTCCCAATTTGCGCCCTTCTTAAACAATGAGGCTGTGTG 419
    |||
DB 380 CACCGCACCAACTGTGCTCCCTCCCACTACGCGCTCCCAACGACGACGCGGCTGTGTG 439
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QY 420 CAACCCCACTCAAGCATTTTGTATATGACCCCAACCGCTTGGGAAAAGATTGATTTTA 479
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DB 440 CAACCGCCCGGAGAGCACTTCAACATGCGGAGCGGCGGCTGTGTCAAGATCGGCATCTA 499
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QY 480 CAGAGAGGATGTCTCCGCTGCTATTTCAAGGGTTCATGCAAAAAGCATGAGGGGT 539
    |||
DB 500 CCGCGGGGATGTGCTGCTCAACTCAAAAGGCTGCTGTGTGAAAGAAAGCGGGGT 559
    |||
QY 540 TAGTTCAATGTGAATGGAGGAGCTATTGAGCTGTATGATGACGAATGTGGGGG 599
    |||
DB 560 GAGGTTCAGATCAACGCGGCGCACTACTGAGCTGTCTCTCCATGTGCGCG 619
    |||
QY 600 TGCTGATTCATCAATCAATGATTTTCAATTAAGGCTCAAAATGATGATGCAATGTC 659
    |||
DB 620 CTGCGGGTCACTCACTGCGGCTTCATCAAGGGTCCGCGACCGGGTGTATGCGCATGTC 679
    |||
QY 660 AAGAAATGGGGTCTTAATTTGCAATGCAATGCGTATTTGATGATCAATCTTGTCTT 719
    |||
DB 680 CCGGAATCGGGGCGTCAACTGCGCAGTCCAAAGCGTCACTCAATGCGCAGACCTGTGTT 739
    |||
QY 720 CAGGTCACCACTCATATGAGAGACAGAGTTTCCAAAGATTTTTCAGTAAATTG 779
    |||
DB 740 CCAAGTACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 799
    |||
QY 780 GACATTCGCGCAACTTTCTTACGCCAGTTCACTTCT 817
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DB 800 GGGGTTGCTGACGCTTTTGACCTCGCAGCACTTCT 837
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RESULT 12

AAC41531
ID AAC41531 standard; DNA; 695 BP.

XX AAC41531;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SRQ ID NO: 32219.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KM promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

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XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
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PR 08-APR-1999; 99US-0128714P.  
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PR 01-JUL-1999; 99US-0141842P.  
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PR 09-JUL-1999; 99US-0142920P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 14-OCT-1999; 99US-0159337P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.
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Query Match 32.2%; Score 350.6; DB 3; Length 1132;
Best Local Similarity 71.9%; Pred. No. 3.2e-69;
Matches 458; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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QY 190 GGGGAGCTTGGGATGGAATCTGTATGCACTGGATGGAAGTCACTGACGCT 249
DB 230 GGTGGAGCTTGGGATGGAATCTGTATGCACTGGATGGAAGTCACTGACGCT 289
QY 250 TTAAGCAGCTTGTATGATGAGCTTCTGTGTGATGAGTCACTGATGATGAT 309
DB 290 TTAAGCAGCTTGTATGATGAGCTTCTGTGTGATGAGTCACTGATGATGAT 349
QY 310 GATTACAAATCAGATCTAGATGATGATGATGATGATGATGATGATGATGAT 369
DB 350 GATCAGCGCGGAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 409
QY 370 AACTTTGCGCTCCCAATTTGCGCTTCTTAACAACATGAGGCTGAGCAACCA 429
DB 410 AACTTTGCGCTCCCAATTTGCGCTTCTTAACAACATGAGGCTGAGCAACCA 469
QY 430 CTGAAGCTTTGATATGCGCCCAACCGCTTGGGAAAGATGATGATGATGATG 489
DB 470 CTGAAGCTTTGATATGCGCCCAACCGCTTGGGAAAGATGATGATGATGATG 529
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QY 610 ATCAATCAGTGTCTATTAAGGCTCAAAAAGTGAATGATGATGATGATGATG 669
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QY 670 GGTTCATATGGAATCAATGATGATGATGATGATGATGATGATGATGATGAT 729
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QY 730 ACCATGATGAGAGACCAAGATTTTCAAGATATGTTTCAAGTAAAGTGAATG 789
DB 770 ACTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829
QY 790 CAAACTTCTCTAGCCCACTTCACTGATGATGATGATGATGATGATGATGAT 826
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DB 830 CAGATTATCTTCCAAAGTTCAGTTTAAAGTTT 866

RESULT 11

ADXS1829
ID ADXS1829 standard; cDNA; 1010 BP.

AC ADXS1829;

XX 21-APR-2005 (first entry)

DE plant full length insert polynucleotide seqid 26569.

XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.

OS Unidentified.

PN US2004034888-A1.

PD 19-FEB-2004.

PF 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

PA (ZHOV/) ZHOV Y.

PA (SCRE/) SCREEN S E.

PA (TABN/) TABASKA J E.

PA (CAOV/) CAO Y.

XX LIAU J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

PI WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 26569; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC <http://seqdata.uspto.gov/sequence.html?DocID:2004034888>. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

SQ Sequence 1010 BP; 179 A; 321 C; 296 G; 214 T; 0 U; 0 Other;

Query Match 30.9%; Score 336.4; DB 13; Length 1010;

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PR 16-APR-1999; 99US-0129845P.
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PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.

XX ACN46900;
XX 02-DEC-2004 (first entry)
XX
DE Cotton primed seed EST Clone ID: L1B3825-005-Q1-K6-G8, SEQ:1661.
XX
XX Cotton; plant; EST; expressed sequence tag; transgenic plant; seed;
XX variety DP50B; library L1B3825; molecular tag; molecular marker;
XX genetic mapping; molecular mapping; seed germination; plant growth;
XX plant quality; plant yield; plant breeding; tissue printing; ss.
XX
XX Gossypium hirsutum.
XX
XX US2004123340-A1.
XX
XX 24-JUN-2004.
XX
XX 12-DEC-2001; 2001US-00021323.
XX
XX 14-DEC-2000; 2000US-0255619P.
XX
XX (DEIK/) DEIKMAN J.
XX (FENG/) FENG P C.
XX (FINC/) FINCHER K L.
XX (ZIEG/) ZIEGLER T E.
XX
XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX
XX WPI; 2004-479808/45.
XX
XX New isolated nucleic acid molecule that encodes a plant protein or its
XX fragment, useful for isolating a variety of agronomically significant
XX genes associated with plant growth, quality or yield, and as molecular
XX tags to map genes.
XX
XX Claim 1; SEQ ID NO 1661; 34pp; English.
XX
XX The invention relates to 17880 cotton expressed sequence tags (ESTs;
XX ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
XX from primed or non-primed seeds from variety DP50B, mature seeds from
XX variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
XX tissue, developing fibres, carpel walls and septa from variety
XX Nucleon33B. The invention also relates to substantially purified
XX proteins or their fragments encoded by nucleic acid molecules of the
XX invention, and to transformed plants having a nucleic acid construct
XX comprising a nucleic acid of the invention. The cotton ESTs are useful as
XX molecular tags to isolate genetic regions, to isolate genes, to map
XX genes, to determine gene function and to determining whether genes are
XX members of a particular gene family. The nucleic acid molecules may be
XX used for isolating a variety of agronomically significant genes
XX associated with plant growth, quality, yield, and could also serve as
XX links in metabolic and catabolic pathways. The nucleic acid molecules are
XX also useful for identifying genes important in initiating and maintaining
XX seed germination or that may be used to mitigate stresses encountered
XX during seed germination. The ESTs additionally enable the acquisition of
XX promoters and cis-regulatory elements which will be useful to express
XX agronomically significant genes in these tissues and/or other tissues,
XX and also permits the acquisition of molecular markers useful in breeding
XX schemes, genetic and molecular mapping, and in cloning of agronomically
XX significant genes. The nucleic acid molecules are further useful for
XX detecting the expression level or pattern of a protein or mRNA and for
XX detecting the presence or quantity of a protein by tissue printing. The
XX present sequence represents a specifically claimed EST isolated from a
XX cotton variety DP50B primed seed cDNA library (L1B3825). The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from the US patent office at
XX seqdata.uspto.gov/sequence.html?docid=US20040123340
XX
XX Sequence 576 BP; 144 A; 136 C; 144 G; 152 T; 0 U; 0 Other;
XX
XX Query Match 33.6%; Score 366.4; DB 13; Length 576;
XX Best Local Similarity 77.3%; Pred. No. 7.4e-73;

Matches 445; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
QY 242 CTGCAGCTTTAAGCACTGCTTATTTAATGATGAGACTCTCTGTGTCAGTCTCAAAAA 301
DB 1 CGGCCCGTGGGGTACTGCTTGTTCATATGAGACTTCATGCGGACATGCTATATAGA 60
QY 302 TTATATGATATTAACAAATGAGACTGATGATGATGATGATGATGATGATGATGATGAT 361
DB 61 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 362 CTGCACAAATCTTTGCTCTCCCAATTTGAGCTTCTCTCAACAAATGAGAGGCTGTGCA 421
DB 121 CAGCAACAAATCTTTGCTCTCTCAATTTGCTCTCTCAACAAATGAGAGGCTGTGCA 180
QY 422 ACCCACTCAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
DB 181 ATCAACCTCCAGCACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 482 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
DB 241 GAGGCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 542 GGTTCAGTGAATGAGAGGAGCACTACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 601
DB 301 GGTTCAGTGAATGAGAGGAGCACTACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 360
QY 602 CTGATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
DB 361 CAGGATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 662 GAATTTGGGCTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
DB 421 GGAATCTGGGAGCTCAATTTGAT 480
QY 722 GGGTCACACCACTGAT 781
DB 481 GGGTCACACCACTGAT 540
QY 782 CATTCGGCCAACTTCTCTAGCCAGTTCAGTTC 817
DB 541 GTTTGGCCAGACTTCTCTAGCAACTCAATTC 576
RESULT 10
AAC38981
ID AAC38981 standard; DNA; 1132 BP.
XX
AC AAC38981;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 22912.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX BP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000BP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.

Db	181	GTNACNGTNACGNCACNAATYTTTGYCCNCCNAATTTGCACTTNCNNAATYAAATYAGN	240
Qy	412	GGCTGTGTCAACCCCACTCAAGCATTTTGTATGTGGCCCAACCCCTGTGGAAAAATT	471
Db	241	GGNTGTGTAAATCCNCCNVTNBARCAATTTTGTATGTGGCCARCCNCGNTGGAAAAATH	300
Qy	472	GGAATTTACAGAGAGAGGATCGTCCCTCGTGCTATTTCAAAGGTTTCATGCAAAAAAGCAT	531
Db	301	GGNAHTHTYMGNGGNGNATHTGNCNCGTNTTTCATCGARCGNCTNCCTGTAAARACAY	360
Qy	532	GGAGGGGTAGGTTCACTAGTGTATGGAGGAGACTTGTAGCTAGTATGATCAGCAAT	591
Db	361	GGNGGNTGNTGTTTWSNGTNAATYGGNMGNATATTTTGARTNGTNTNTNATHMSNAAY	420
Qy	592	GTGGGGGGTGTGATTCATCCATCAATGTTTCATTAAAGCTCAAAAACGTGATGATG	651
Db	421	GTNGNGGNGCNGGMSNATHCARBSNGTNTTATTAARAGGMSNABARACGNTGATG	480
Qy	652	GCAATGTCAAGAAATTTGGGTTCTAATTTGGCAATCCAT	690
Db	481	GCNATGWSNMGNAATYTGCGGMSNAATYTGCCAAWSNAAY	519

RESULT 8

ACN46903
ID ACN46903 standard; cDNA; 601 BP.

AC ACN46903 ;

DT 02-DEC-2004 (first entry)

DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-K6-H7, SEQ:1684.

KM	Cotton; plant; EST; expressed sequence tag; transgenic plant; seed
KM	variety DP508; library LIB3825; molecular tag; molecular marker;
KM	genetic mapping; molecular mapping; seed germination; plant growth;
KM	plant quality; plant yield; plant breeding; tissue printing; ss-

OS *Gossypium hirsutum.*

PN US2004123340-A1.

PD 24-JUN-2004.

PF 12-DEC-2001; 2001US-00021323.

PR 14-DEC-2000; 2000US-0255619P.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;

DR WPI; 2004-479808/45.

PT New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.

PS Claim 1; SEQ ID NO 1684; 34pp; English.

CC The invention relates to 17880 cotton expressed sequence tags (ESTs);
CC ACNA52220-ACN63509). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Bonwell 96 Field, and aridocrocin tissue, gynoeceum
CC tissue, developing fibres, carpal walls and septa from variety
CC Nucotcon33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct

CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determining whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a
CC cotton variety D50B primed seed cDNA library (U193825). The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?IDocID=US20040123340
XX
XX Sequence 601 BP; 153 A; 137 C; 150 G; 161 T; 0 U; 0 Other;

SQ Sequence 601 BP; 153 A; 137 C; 150 G; 161 T; 0 U; 0 Other;

Query Match 34.1%; Score 371.6; DB 13; Length 601;

Matches 452; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

242 CTGCAGCTTTAAGCACTGCCATTATTATGATGGAGCTTCCTGTGGTCAGTGCTACAAA 301

Db 1 CGGCCCGGTGGGTA CTGCC TTGTT CATAATG GAGCTT CATGCG GACATGCTATA GA 60

302 TTATATGTGATTACAATCAGACTTAGATGGTGCATCAAGGAGATCTGTAACCGTAA 36

Db 61 TCATGTGACTATCAGACAGATCCAGATGGTGATTAAGAAGACATCCGTGACCATTA 120

362 CTGCCACAACCTTTGGCCCTCCCAATTTCGCCCTTCCTAACACAACATGGAGGCTGTGCA 421

Db 121 CAGCAACAACCTTTGTCTCTACTTTGCTCTCCCAACAATGCCGAGGCTGTCA 180

422 ACCCACCACCTCAAGCATTTTGATATGCCCAACCCGCTTGGGAAAGATTGGTATTACA 481

Db 181 ATCCACCCCTCCAGCACTTGGCATGGCTCAGCCTGCCCTGGGAAGAATGGTATCTACA 240

482 GAGGAGGATCGTCCCGTGCTATTCAAGGGTTCATGC AAAAAGCATGGAGGGGTTA 541

Db 241 GAGCGGAATTGTGCCCGTTTGTTCCAAAGGTTCTTGCAGAAGCATGGTGGAGTGA 300

542 GGTTCAGTGTGAATGGAGGACTTTCAGCTAGTATTGATCAGCAATGTGGGGGTG 601

Db 301 GGTTCACGATCAATGGAAGAGACTATTTCGAGCTTGTATGATTAGCAATGTTGGTGGC 360

602 CTGGATCCATCCAATCAGTGTTCATTAAAGCTCAAAACTGGATGGCAATGTCAA 663

Db 361 CAGGATCTATCCAGTCTGTGTCCATCAAGGCTCCAAACTGGGTGATGGCAATGTCAA 420

662 GAAATTGGGTTCTAATTGGCAATCCAATGCGTATTGAATGGTCAATCTTTGTCCTTCA 721

Db 421 GGAAGTGGGAGCTAACTGGCAATCCAAATGCCCTATCTCAATGGCCAAATCATTGTGTTCA 480

722 GGGTCACCACTGATGGAGAGACCAGAGTTTCCAGATATTGTTCCAGTAAGTTGCA 781

Db 481 GGGTCACCACTACTGATGGTGTGACTCGTCTATTTCCTGACATCGTGCCTGCAAAATGGG 540

782 CATTGGCCAAACTTTCTCTAGCCAGTTCAGTTCCTAGCTGATTA 827

Db 541 GTTTGGCCAGACTTCTCTAGCAACTACATTCCTAGATTTAGTA 586

CCCCCEC

RESULT 9

ID ACN46900 standard; cDNA: 576 BP.

PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
XX Claim 1; SEQ ID NO 2291; 134pp; English.
XX
CC This invention relates to a novel method for altering one or more plant
CC characteristic. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreduplication, biochemistry, signal
CC transduction, storage lipid mobilization and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC transcription factors. This polynucleotide sequence is thale cress cDNA
CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa
CC transcription factor, given in an exemplification of the invention.
XX

Sequence 759 BP; 187 A; 153 C; 194 G; 225 T; 0 U; 0 Other;

Query Match 35.0%; Score 380.8; DB 12; Length 759;
Best Local Similarity 71.3%; Pred. No. 4.5e-76;
Matches 502; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 116 ATGCTCTTCACCTTGTGATGACCAAGCCCACTTTTATGAGGAGTATGATG 175
DB 56 ATGCGTTTAGCCCTTCTGTTTAATGATGTCACGCTACATTTATGAGGAAGTACG 115
QY 176 CTTGAGGAATATGAGGAGGAGCTTGTGAGTATGAGGAATCTGTATGCACTGGGTATGGA 235
DB 116 CTTCTGGAACAAAGGAGGAGCTTGTGATGAGGAGATCTTACTCGCGAGGATGAGGA 175
QY 236 CTGAACTGACGCTTTAAGCACTGCTTATTTATGATGAGGCTTCTGTGATGATGCT 295
DB 176 CATGACGCGGCGGTTAAGACCGGCTGTCTTCAACAGAGAGCTTCTGTGAGGAATGCT 235
QY 296 ACAAATTTATATGATGATTAACAATTCAGACTCTGATGATGATGATCAAAAGAGATCTGTAA 355
DB 236 ATGAGTAACGTGTGATCAAGCGCGAGCACTCAGCGTGTCTTGAAGAGAGCTTCTGTGG 295
QY 356 CCGTAATGCGCAAACTTTTGGCCCTCCCAATTTGCGCTTCTTAACAACAATGAGAGCT 415
DB 296 TTATTTACAGCACTAATCTTTTGGCCCAACAACTTTGCTTAAACAACAACGATGCTT 355
QY 416 GGTCAACCAACCACTCAAGCACTTTTGTATGAGCCCAACCGCTTGGGAAAAGATGTTGTA 475
DB 356 GGTGCAATCCGCGCTTAAACATTTGCAATGCAACAGCAACCGCTTGGGAAAAGATGCGAA 415
QY 476 TTTACAGAGGAGGATGCTCCCGTGTATTTCAAAAGGTTCAATGCAAAAAGCATGAGAG 535
DB 416 TTTACAGAGGAGGATGCTCCCGTGTATTTCAAAAGAGTGTATTAACAAGAGAGAG 475
QY 536 GGGTTAGGTTCAATGATGATGAGGAGCACTATTGAGCTAGTATGATCAACAATGTGG 595
DB 476 GAAATTGATTCAGAAATTAAGGAGAGACATCTTCGAGCTAGTGAATATTCAAAAATGTAG 535
QY 596 GGGGTCTGGATCATTCATCAATGATGTTTCAATTAAGGCTCAAAAAGCATGATGATGCA 655
DB 536 GAGGAGAGAGGTTTATTAATCTGTATCTATCAAAAGGATCAAAAGATCGTGTGTTAGCA 595
QY 656 TGTCAAAATTTAGGTTCTTAATTTGCAATCAATGCGATTTGAAATGATCAATCTTTGT 715
DB 596 TGTCTGTAACTGGGAGCTAATTTGGCAATCGAATGTTATCTAGANTGGTCAAGCTCTCT 655
QY 716 CCTTCAAGGCTACCACTGATGAGAGACAGAGTTTCCAAAGATATTTGTTCCAGTAA 775

DB 656 CTTTCTCACTATACACTACTGATGATGCTACTAGAGCTTTCTCAATGTTGTTCTTCT 715
QY 776 GTTGAACATTGGCCAAACTTCTCTAGCCCACTGATTTCA 819
DB 716 CTTGCTCTTTTGACAGATTTATTTCCAAAGCTGATTTTAA 759

RESULT 7
ADV03864
ID ADV03864 standard; DNA; 519 BP.
XX
AC ADV03864;
XX
DT 21-APR-2005 (first entry)
XX
DE Soybean expansin, GmEXP1, probe, SEQ ID 5.
XX
KW GmEXP1; expansin; plant; root; development; probe; ss.
XX
OS Glycine max.
XX
PN KR2004084186-A.
XX
PD 06-OCT-2004.

XX 27-MAR-2003; 2003KR-00019069.
XX
XX 27-MAR-2003; 2003KR-00019069.
XX
XX (UYSE-) UNIV SEOUL NAT IND FOUND.
XX
XX Ahn JH, Choi YD, Lee DG, Lee JS, Song SG,
XX WPI; 2005-108897/12.

PT Gene controlling root development of plant and method for manipulating
PT root development of plant using the same to improve phenotype of plant
PT related to root development and facilitate its growth.
XX
XX

Example 1; SEQ ID NO 5; 27pp; Korean.

CC The present invention relates to soybean gene GmEXP1 coding sequence
CC (ADV03864), which encodes the protein expansin (ADV03861), which in turn
CC controls plant root development. The invention also relates to a method
CC for manipulating plant root development using GmEXP1 expansin, to improve
CC the phenotype of a plant related to root development, and facilitating
CC the growth of it. Also disclosed are: recombinant vector pGA643/GmEXP1,
CC which contains gene GmEXP1; and a transformed bacterium produced by
CC transforming a bacterium with the recombinant vector pGA643/GmEXP1. The
CC method for facilitating the root development of a plant comprises
CC inserting the gene GmEXP1 into the expression vector, and introducing the
CC expression vector into the plant. The present sequence is a probe used in
CC an example from the invention.
XX

Sequence 519 BP; 88 A; 45 C; 111 G; 68 T; 0 U; 207 Other;

Query Match 34.5%; Score 376.2; DB 14; Length 519;
Best Local Similarity 60.1%; Pred. No. 4.4e-75;
Matches 312; Conservative 113; Mismatches 94; Indels 0; Gaps 0;

QY 172 GATGCTTCAAGAACTATGAGGAGGAGCTTGTGATGAGGAATCTGTATGCAACTGGTAT 231
DB 1 GATGCTTCAAGAACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
QY 232 GGAATCAAGAACTGACGCTTTAAGCACTGCTTATTTAAGAGGAGCTTCTGTGCTGAG 291
DB 61 GGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 292 TGTCAAAATTTATGATGATTAACAATCACTAGATGAGGATGAGGAGGAGGAGGAGGAG 351
DB 121 TGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 352 GTAACCGTAATGCAAAACTTTTGGCTCCCAATTTGCGCTTCTTAACAACAATGGA 411

Db 388 AACGGTGGTGTGCAATCCGCCGCTTAAACATTTGCACATGGCACAAACCCGCTTGGAA 447
 QY 466 AAGATTGATTTTACAGAGAGGATCGTCCCGCTATTTTCAAAAGGTTCCATGCAAA 525
 Db 448 AAGATCGAATTTACAGAGAGGATCGTCCCGCTATTTTCAAAAGGTTCCATGCAAA 507
 QY 526 AAGCATGAGAGGGTGTAGTTGATGATGATGAGAGGATCTTGAATGATTTGATG 585
 Db 508 AAGAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567
 QY 586 AAGCATGAGAGGGTGTAGTTGATGATGATGATGATGATGATGATGATGATGATG 645
 Db 568 CAAAATGTAGAGAGACAGGTTCTATTTAACTGTATTCATCAAGAGATCAAGACTGT 627
 QY 646 TGGATGAGCATGTCAGAAATTTGGGGGTTTGAATTTGGCAATGCGATTTTGAATG 705
 Db 628 TGGTAAAGCATGCTGTGATTTGGAGAGCTAATTTGGCAATGCGATTTTGAATG 687
 QY 706 CATCTTTTGTCTTCAAGGGTCAACCACTGATGAGAGACAGAGTTTCCAAAGATTT 765
 Db 688 CAAGCTCTCTCTTCTCTATTAACAATGATGATGATGATGATGATGATGATGATG 747
 QY 766 GTTCCAGTAAGTGAACATTCGACCAACTTTCTTACCCAGTTCACTTCAAGCTGAT 825
 Db 748 GTTCTTCTTCTGCTTGTGAGACAGATTTATTTTCCAACTGATGATTTTAAAGTTT 807
 QY 826 T 826
 Db 808 T 808

RESULT 5
 ADY03866
 ID ADY03866 standard; RNA; 389 BP.

XX ADY03866;
 AC 21-APR-2005 (first entry)
 DT Soybean expansin, GmEXPL, RNA sense probe, SEQ ID 7.
 DE GmEXPL; expansin; plant; root; development; probe; ss.
 XX Glycine max.
 OS KR2004084186-A.
 PN 06-OCT-2004.
 PD 27-MAR-2003; 2003KR-00019069.
 PF 27-MAR-2003; 2003KR-00019069.
 PR (UYSE-) UNIV SEOUL NAT IND FOUND.
 PA Ahn JH, Choi YD, Lee DG, Lee JS, Song SG;
 PI WPI; 2005-108897/12.
 DR WPI; 2005-108897/12.
 XX Gene controlling root development of plant and method for manipulating
 PT root development of plant using the same to improve phenotype of plant
 PT related to root development and facilitate its growth.
 PS Example 7; SEQ ID NO 7; 27bp; Korean.
 XX The present invention relates to Soybean gene GmEXPL coding sequence
 CC (ADY03866), which encodes the protein expansin (ADY03861), which in turn
 CC controls plant root development. The invention also relates to a method
 CC for manipulating plant root development using GmEXPL expansin, to improve
 CC the phenotype of a plant related to root development, and facilitating
 CC the growth of it. Also disclosed are: recombinant vector pG643/GmEXPL,
 CC which contains gene GmEXPL; and a transformed bacterium produced by
 CC transforming a bacterium with the recombinant vector pG643/GmEXPL. The

CC method for facilitating the root development of a plant comprises
 CC inserting the gene GmEXPL into the expression vector, and introducing the
 CC expression vector into the plant. The present sequence is a probe used in
 CC an example from the invention.

SQ Sequence 389 BP; 110 A; 91 C; 69 G; 0 T; 119 U; 0 Other;

Query Match 35.7%; Score 389; DB 14; Length 389;

Best Local Similarity 69.4%; Pred. No. 5.3e-78;

Matches 270; Conservative 119; Mismatches 0; Indels 0; Gaps 0;

QY 603 TGGATCCATCCATCGTGTTCATTAAGCTTCAAAAGCTGATGATGATGATGATGATG 662
 Db 1 UGAGUCCACCAUCCAUUGUUCUUAAGGCUUAAAACUGAGUAGUAGUAGUAGUAG 60
 QY 663 AAATGGGGGTTCTTAATTTGGCAATCGATGATGATGATGATGATGATGATGATGATG 722
 Db 61 AAATUGGGGUCUUAUUGGCAUCCAUUGGCUUUAUUGGCAUCCAUUGGCUUUG 120
 QY 723 GGTCAACCACTGATGAGAGACAGAGTTTCCAAAGATTTTCCAGTAAGTTGAG 782
 Db 121 GGUCAACCACTGATGAGAGACAGAGTTTCCAAAGATTTTCCAGTAAGTTGAG 180
 QY 783 ATTGGCCCAACTTTCTTACCCAGTTCACTTCAAGCTGATGATGATGATGATGATG 842
 Db 181 AUTCAGCCCAAACTTCTTACCCAGTTCACTTCAAGCTGATGATGATGATGATGATG 240
 QY 843 AGGCTGAGAGCGGCTTTTATTTTATTTTACTGAGAGTCCGCCACCTTCTTGTG 902
 Db 241 ACAGCUGAGGCGGCUUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 300
 QY 903 TTGATTTATTTCCATCACTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 962
 Db 301 UUGAUUUAUCCAUCAACUCCAUCAAGCCUUAUUAAGGCAUUAUUAUUAUUA 360
 QY 963 ATCAATCACCATCATATCATATGACTT 991
 Db 361 AUCAUACACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 389

RESULT 6
 ADN74396
 ID ADN74396 standard; cDNA; 759 BP.

XX ADN74396;
 AC 15-JUL-2004 (first entry)
 DT Thale cress cDNA repressed in E2Fa/Dpa expressing plants SegID 2291.
 XX gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
 KW growth regulator; animal feed product; thale cress;
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
 XX Arabidopsis thaliana.
 OS WO2004035798-A2.
 PN 29-APR-2004.
 PD 20-OCT-2003; 2003WO-BP011658.
 PF 18-OCT-2002; 2002EP-00079408.
 PR (CROP-) CROPDESIGN NV.
 PA Inze D, De Veylder L, Vlieghe K;
 PI WPI; 2004-348466/32.
 DR P-PSDB; ADN74397.
 XX Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of

PR 23-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140655P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145122P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145951P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147392P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 26-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.

PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 36.1%; Score 393; DB 3; Length 980;
Best Local Similarity 71.6%; Pred. No. 8.3e-79;
Matches 516; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 106 ATCACTTACTATGCTCTTCTACCTCTGATGACCAACGCCATGCACTTTTATGGC 165
DB 88 ATTGCTGTGATGCTGTTAAGCTTCTGTTAACTAATGGCAACGCTACATTCTATGGA 147
QY 166 GGTAGTGAATGCTTACAGAACTATGCGGAGCTTGGGTATGGAATCTGTATGCACT 225
DB 148 GGAATGACGCTTCTGGAACAAATGGGTGAGCTTGGGTACGAGATCTTTACTCGCGC 207
QY 226 GGGTATGGAATGAACTGAGCTTTAAGACCTGCTTATTTATGATGAGGCTTCTCTGT 285
DB 208 GGGTACGGGCAATGACGGGAGGTTAAGACGCTTGTCAACGAGAGCTTCTTGC 267
QY 286 GGTCAAGTCAACAAATTTATGATTTCAATCAAGACTCTAGATGGTGCATCAAGGA 345
DB 268 GGAATGCTATATGAGTAAGTGTGATCAGCGCGGACTCAAGGTGTCTTGAAGGA 327
QY 346 AGATCTGTAACTTAATGCAAACTTTGGCTTCCCAATTTGGCCCTTCTTAAC 405
DB 328 GCTTCTGTGTATTTAAGCCACTAATCTTTGGCCACAACTTTGCTTGAACAAC 387
QY 406 AATGAGGCTGTGCAACCACTCAAGACTTTGATTTGGCCCAACCCGCTTGGGA 465

CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX
 XX
 XX Sequence 1134 BP; 322 A; 244 C; 234 G; 334 T; 0 U; 0 Other;

Query Match 91.9%; Score 1001.2; DB 13; Length 1134;
 Best Local Similarity 99.6%; Pred. No. 3.8e-216;
 Matches 1014; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 8 CTTCAACCTCTCATTCATTAGGACATTGAGCAAGCAAGAAAAAATGGCAAAATCATGCG 67
 DB 117 CTTCAACCTCTCATTCATTAGGACATTGAGCAAGCAAGAAAAAATGGCAAAATCATGCG 176
 QY 68 TTGTTTTGGGTAGCCTTCATTGATGATGCTGTTTCAAAATCACTACCTATGCTTCTCAC 127
 DB 177 TTGTTTTGGGTAGCCTTCATTGATGATGCTGTTTCAAAATCACTACCTATGCTTCTCAC 236
 QY 128 CTTCTGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 187
 DB 237 CTTCTGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 296
 QY 188 TGGGGGGAGGCTTGAGGGGATGAGGAACTGTATGCAACTGTATGAACTGAAGCAAGCAAG 247
 DB 297 TGGGGGGAGGCTTGAGGGGATGAGGAACTGTATGCAACTGTATGAACTGAAGCAAGCAAG 356
 QY 248 CTTTAAAGCACTGCTTATTTATGATGAGCACTTCTGTGTCAGTGTACAAATATATAT 307
 DB 357 CTTTAAAGCACTGCTTATTTATGATGAGCACTTCTGTGTCAGTGTACAAATATATAT 416
 QY 308 GTGATTAACAATCAAGCTCTAGATGTCATCAAGAAAGATCTGTAACTGTAACTGTAACTGT 367
 DB 417 GTGATTAACAATCAAGCTCTAGATGTCATCAAGAAAGATCTGTAACTGTAACTGTAACTGT 476
 QY 368 CAAACTTTGCGCCCAATTTGGCCCTTCTTAACAACAATGAGGGGTGTGCAACCCAC 427
 DB 477 CAAACTTTGCGCCCAATTTGGCCCTTCTTAACAACAATGAGGGGTGTGCAACCCAC 536
 QY 428 CACTCAAGCAATTTGATGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 487
 DB 537 CACTCAAGCAATTTGATGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 596
 QY 488 GGATGCTCCCGTGCTATTTCAAAAGGGTTCATGCAAAAAGCATGAGGGGTTAGGTTCA 547
 DB 597 GGATGCTCCCGTGCTATTTCAAAAGGGTTCATGCAAAAAGCATGAGGGGTTAGGTTCA 656
 QY 548 GTGTGAATGGGAGGACTACTTGTAGCTATGATGATGATGATGATGATGATGATGATGATG 607
 DB 657 GTGTGAATGGGAGGACTACTTGTAGCTATGATGATGATGATGATGATGATGATGATGATG 716
 QY 608 CCATCAATCAAGTTCATTAAGAGCTCAAAAATCGATGATGATGATGATGATGATGATGATG 667
 DB 717 CCATCAATCAAGTTCATTAAGAGCTCAAAAATCGATGATGATGATGATGATGATGATGATG 776
 QY 668 GGGGTTCTAATGGCAATCAATGCGTATTTGAATGATGATGATGATGATGATGATGATGATG 727
 DB 777 GGGGTTCTAATGGCAATCAATGCGTATTTGAATGATGATGATGATGATGATGATGATGATG 836
 QY 728 CACACCTGATGAGAGCAAGAGTTTCCAAGATATGTTCCAGTAAAGTTGAGCAATTCG 787
 DB 837 CACACCTGATGAGAGCAAGAGTTTCCAAGATATGTTCCAGTAAAGTTGAGCAATTCG 896

QY 788 GCCAACTTCTCTAGCCCAAGTTCAGTCTAAGCTGATTAACAGATAAACCAACCAAGCGC 847
 DB 897 GCCAACTTCTCTAGCCCAAGTTCAGTCTAAGCTGATTAACAGATAAACCAACCAAGCGC 956
 QY 848 TGAGGGGTGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 907
 DB 957 TGAGGGGTGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1016
 QY 908 TATTCATCACTCCAGCCCTCTATCAAGGCAATTAATTTATCAATTAAT ACATCA 966
 DB 1017 TATTCATCACTCCAGCCCTCTATCAAGGCAATTAATTTATCAATTAATTAATCAATCA 1076
 QY 967 ATCACCATCATATCATATATAGCTTGTATATCAAAATTAATTTCAAGTTAAATTT 1024
 DB 1077 ATCACCATCATATCATATATAGCTTGTATATCAAAATTAATTTCAAGTTAAATTT 1134

RESULT 3
 AAD03712
 ID AAD03712 standard; cDNA; 1103 BP.

XX
 XX AAD03712;
 AC
 XX
 DT 19-JUN-2001 (first entry)

XX
 DE Tomato seed expansin, LeExp8, cDNA for controlling seed germination.
 XX
 XX Tomato; endo-beta-mannanase; Lycopersicon esculentum mannanase2; LeMAN2;
 KM polygalacturonase; PG; LexPG1; cellulase; arabinosidase; LeAR1;
 KM xyloglucan endotransglycosylase; XET; LexXT4; expansin; LeEXP4; LeEXP8;
 KM LexXP10; hydrolase; endosperm cap; tissue weakening; radicle growth;
 seed germination; ss.

XX
 OS Lycopersicon esculentum.
 XX
 FH Key Location/Qualifiers
 FT CDS 39..812
 FT /*tag= a
 FT /product= "Tomato seed expansin, LeExp8"

PN W0200123530-A1.

XX
 PD 05-APR-2001.

XX
 PF 29-SRP-2000; 2000MO-US026884.

XX
 PR 30-SRP-1999; 99US-00410191.

XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Bradford KJ, Chen F, Dahal P, Downie B, Nonogaki H;

XX
 DR WPI; 2001-266144/27.

XX
 DR P-PSDB; AAE00413.

XX
 PT Novel nucleic acid sequences isolated from germinating seeds encoding

XX
 PS polypeptides that are useful to control seed germination in plants.

XX
 Claim 4; Page 49; 63bp; English.

XX
 CC The present invention relates to enzymes such as seed-specific endo-beta-
 CC mannanase (e.g., Lycopersicon esculentum (Le) MAN2), polygalacturonase
 CC (PG) (e.g., LexPG1), cellulases such as Cel55 and Cel68, arabinosidase
 CC (e.g., LeAR1), xyloglucan endotransglycosylase (XET) (e.g., LexXT4) and
 CC expansins such as LexXP4, LexXP8 and LexXP10 isolated from germinating
 CC seeds. All these enzymes are expressed initially in the endosperm caps
 CC and are associated with cell wall hydrolysis. These enzymes are
 CC associated with weakening of tissues surrounding the embryo and/or
 CC initiating radicle growth. The control of expression of these endogenous
 CC genes is therefore a convenient means for controlling seed germination.
 CC The present sequence is tomato seed expansin, LeExp8, cDNA. Expansins are
 CC extracellular proteins that facilitate cell wall extension

(ADY03860), which encodes the protein expansin (ADY03861), which in turn controls plant root development. The invention also relates to a method for manipulating plant root development using GmEXP1 expansin, to improve the phenotype of a plant related to root development, and facilitating the growth of it. Also disclosed are: recombinant vector pDA643/GmEXP1, which contains gene GmEXP1; and a transformed bacterium produced by transforming a bacterium with the recombinant vector pDA643/GmEXP1. The method for facilitating the root development of a plant comprises: CC inserting the gene GmEXP1 into the expression vector, and introducing the expression vector into the plant.

XX Sequence 1089 BP; 323 A; 225 C; 226 G; 315 T; 0 U; 0 Other;

Query Match 100.0%; Score 1089; DB 14; Length 1089;
Best Local Similarity 100.0%; Pred. No. 5 6e-236;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GCACGAGCTTCAACCTTCATCATTTAGGCAATTCAGCAAGCAAGAAAAAATGGGCAAA 60
DB 1 GCACGAGCTTCAACCTTCATCATTTAGGCAATTCAGCAAGCAAGAAAAAATGGGCAAA 60
QY 61 ATATAGCTGTTTGGGTAGCTCATTGATTAATGCTGTTTCAATCACTACTATGCTC 120
DB 61 ATCATGCTTGTGTTGGGTAGCTCATTGATTAATGCTGTTTCAATCACTACTATGCTC 120
QY 121 TTCTCACTTCTGGATGAGCAACGCGCATGTCATTTTATGGGGGTAGTGAATGCTTCA 180
DB 121 TTCTCACTTCTGGATGAGCAACGCGCATGTCATTTTATGGGGGTAGTGAATGCTTCA 180
QY 181 GGAATATGAGGGGAGCTGTGGTATGAGGATCTGATGCACTGGGTATGGAATGCA 240
DB 181 GGAATATGAGGGGAGCTGTGGTATGAGGATCTGATGCACTGGGTATGGAATGCA 240
QY 241 ACTGCACTTTAAGCACTGCTTATTATGATGAGAGCTTCTGTGCTCAGTCTACAA 300
DB 241 ACTGCACTTTAAGCACTGCTTATTATGATGAGAGCTTCTGTGCTCAGTCTACAA 300
QY 301 ATTATATGATTAACAATCAGACTGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 ATTATATGATTAACAATCAGACTGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 ACTGCAACAACTTTGCTCCCTCCCAATTTGCTCCCTCTTCAACAACAATGAGGCTG 420
DB 361 ACTGCAACAACTTTGCTCCCTCCCAATTTGCTCCCTCTTCAACAACAATGAGGCTG 420
QY 421 AACCCACACTCAAGCACTTTGATATGAGCCCAACCGCTTGGAAAAAGATTGATTTAC 480
DB 421 AACCCACACTCAAGCACTTTGATATGAGCCCAACCGCTTGGAAAAAGATTGATTTAC 480
QY 481 AGAGGAGGAGTCTCCCGCTGATTTCAAAAGGCTTCAAGCAAAAGCAATGAGGGGTT 540
DB 481 AGAGGAGGAGTCTCCCGCTGATTTCAAAAGGCTTCAAGCAAAAGCAATGAGGGGTT 540
QY 541 AGGTTCAATGATGATGAGGAGGAGTCTTGAAGTATGATGATGATGATGATGATGATG 600
DB 541 AGGTTCAATGATGATGAGGAGGAGTCTTGAAGTATGATGATGATGATGATGATGATG 600
QY 601 GCTGATTCATCAATCAGTGTTCATTTAAAGGCTCAAAAAGTGAATGAGGAGTCA 660
DB 601 GCTGATTCATCAATCAGTGTTCATTTAAAGGCTCAAAAAGTGAATGAGGAGTCA 660
QY 661 AGAAATTTGGGTTCTAATTTGGCAATCCAAATGATTTGAATGATTTGCTCTTC 720
DB 661 AGAAATTTGGGTTCTAATTTGGCAATCCAAATGATTTGAATGATTTGCTCTTC 720
QY 721 AGGTTCAATGATGATGAGGAGGAGTCTTGAAGTATGATGATGATGATGATGATGATG 780
DB 721 AGGTTCAATGATGATGAGGAGGAGTCTTGAAGTATGATGATGATGATGATGATGATG 780
QY 781 ACATTTGGGCAAACTTTCTAGCCAGTTCAGTTCATGATTTCAATTAACCAAC 840
DB 781 ACATTTGGGCAAACTTTCTAGCCAGTTCAGTTCATGATTTCAATTAACCAAC 840

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QY 841 CAAGGCTGAGGCGTCTTTTATTTATTTAATGAGAGTCCCGCCACCTTCTTGG 900
DB 841 CAAGGCTGAGGCGTCTTTTATTTATTTAATGAGAGTCCCGCCACCTTCTTGG 900
QY 901 TTTTGAATTTTCCCAATCACTCAAGCCCTCATCAAGGCAATTAATTTCAATATA 960
DB 901 TTTTGAATTTTCCCAATCACTCAAGCCCTCATCAAGGCAATTAATTTCAATATA 960
QY 961 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1020
DB 961 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1020
QY 1021 AATTAATTTATCTATTAATTTGTTAATATCAATTAATGATGAGTCAAAAAA 1080
DB 1021 AATTAATTTATCTATTAATTTGTTAATATCAATTAATGATGAGTCAAAAAA 1080
QY 1081 AAAAAAAAA 1089
DB 1081 AAAAAAAAA 1089

```

RESULT 2

ADX27747
ID ADX27747 standard; cDNA; 1134 BP.

ADX27747:

21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 10567.

KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

OS Unidentified.

PN US2004034888-A1.

PD 19-FEB-2004.

PF 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985676.

PA (LIU/) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABAS/) TABASKA J E.

PA (CAO/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

WIPI; 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

PS Claim 1; SEQ ID NO 10567; 15BP; English.

CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2006, 09:02:51 ; Search time 696 Seconds
(without alignments)
10427.946 Million cell updates/sec

Title: US-10-660-499A-1

Perfect score: 1089

Sequence: 1 gccacgagcttcaacctctca.....aaaaaaaaaaaaaaaa 1089

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1089	100.0	1089	14	ADY03860 Soybean e
2	1001.2	91.9	1134	13	Adx27747 Plant full
3	427.4	39.2	1103	4	AdAD03712 Tomato se
4	393	36.1	980	3	AAC41263 Arabidops
5	389	35.7	389	14	ADY03866 Soybean e
6	380.8	35.0	759	12	Adm74396 Thale cre
7	376.2	34.5	519	14	ADY03864 Soybean e
8	371.6	34.1	601	13	ACN46903 Cotton pr
9	366.4	33.6	576	13	ACN46900 Cotton pr
10	350.6	32.2	1132	3	AAC38981 Arabidops
11	336.4	30.9	1010	13	ADX51829 Plant full
12	335	30.8	695	3	AAC41531 Arabidops
13	334.8	30.7	1029	13	ADX34192 Plant full
14	323.8	29.7	1053	13	ADX54060 Plant full
15	323.2	29.7	634	10	ADK59694 Plant DNA
16	295.6	27.1	753	8	ADA69467 Rice gene
17	293.8	27.0	789	8	ADA69924 Rice gene
18	288.8	26.5	956	13	ADX27589 Plant full
19	282.6	26.0	1455	13	ADX13859 Plant full

20	278.6	25.6	681	2	AA13320 Cucumber
21	278.6	25.6	681	6	ABA97162 C. sativu
22	278.6	25.6	684	6	ABA97161 C. sativu
23	271	24.9	768	6	ABZ13241 Arabidops
24	270.6	24.8	904	12	ADJ39951 Plant cDN
25	269	24.7	269	14	ADY03865 Soybean e
26	268	24.6	1153	12	Adi61916 Cotton fi
27	268	24.6	1153	12	AA156403 Cotton fi
28	266.2	24.4	1167	4	AAAD03713 Tomato se
29	264	24.2	753	6	ABZ12286 Arabidops
30	259.6	23.8	1302	13	ADX14145 Plant full
31	259.4	23.8	780	3	AAC50628 Arabidops
32	259.4	23.8	1198	3	AAC33521 Arabidops
33	259.4	23.8	1233	3	AAC30633 Arabidops
34	257.8	23.7	1276	13	ADT15760 Plant cDN
35	254	23.3	768	11	ACL26574 Rice abio
36	251.6	23.1	1365	3	AAC47991 Arabidops
37	251.4	23.1	1236	3	AAC40035 Arabidops
38	250.4	23.0	1212	3	AAC45165 Arabidops
39	248.6	22.8	747	6	ABZ13264 Arabidops
40	248.6	22.8	1032	13	ADX28373 Plant full
41	248.6	22.8	1324	3	AAC47530 Arabidops
42	248.6	22.8	1326	3	AAC40169 Arabidops
43	247	22.7	822	10	ADK59692 Plant DNA
44	245.2	22.5	757	10	ADK59697 Plant DNA
45	244.2	22.4	1284	13	ADR59884 Cotton CD

ALIGNMENTS

RESULT 1	
ADY03860	ADY03860 standard; cDNA; 1089 BP.
ID	ADY03860;
AC	ADY03860;
XX	
XX	21-APR-2005 (first entry)
DT	
XX	
DE	Soybean expansin, GmEXPL, coding sequence, SEQ ID 1.
XX	
KW	GmEXPL; expansin; plant; root; development; gene; sr.
XX	
OS	Glycine max.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	52..819
FT	/*tag= a
FT	/product= "GmEXPL expansin"
XX	
XX	KR2004084186-A.
PN	
XX	
PD	06-OCT-2004.
XX	
XX	
XX	27-MAR-2003; 2003KR-00019069.
PF	
XX	
PR	27-MAR-2003; 2003KR-00019069.
XX	
XX	(UYSR-) UNITV SEOUL NAT IND FOUND.
PA	
XX	
XX	Abn JH, Choi YD, Lee DG, Lee JS, Song SG;
PI	
XX	
XX	WPI; 2005-108897/12.
DR	
DR	P-PSDB; ADY03861.
DR	GENBANK; AF516879.
XX	
XX	Gene controlling root development of plant and method for manipulating
PT	root development of plant using the same to improve phenotype of plant
PT	related to root development and facilitate its growth.
XX	
PS	Claim 5; SEQ ID NO 1; 27pp; Korean.
XX	
CC	The present invention relates to Soybean gene GmEXPL coding sequence

QY 596 GGGGTCTGATTCATTCATCACTGTTCACTTAAAGCTCAAAACTGATGATGCGAA 655
 |||||
 DB 212 CTGGGCTGATTCATTCATCACTGATTCATCAAGGCTCCCGACAGTTGATGCGCA 153
 |||||
 QY 656 TGTCAAGAAATGGGGTCTCAATTTGGCAATCCAAATGATTTGAATGGTCATCTTTG 715
 |||||
 DB 152 TGTTCAGAACTGGGAGCTACTGCGAGTCTAATGCTAATCTCAATGGCCAGTCTGT 93
 |||||
 QY 716 CCTTCAGGGTCAACCACTGATGAGAGACAGAGTTTCCAAGATATTTCCAGTAA 775
 |||||
 DB 92 CTTCAAGGTCAACCACTGATGAGTGAACCAAGATTCAGCAATGTTGTCTTCAG 33
 |||||
 QY 776 GTTGAATTCGGCCAACTTTCTTAGCCCA 807
 |||||
 DB 32 ATTGGGGTTTGTGTGACACCTTCTTAGCTCA 1
 |||||

RESULT 14
 CX018002/c 733 bp mRNA linear EST 07-DEC-2004
 LOCUS EST 1711 wild type Ugni blanc SSH library Vitis vinifera cDNA clone
 DEFINITION 3596 UB_S9_F11, mRNA sequence.
 ACCESSION CX018002
 VERSION CX018002.1 GI:56409750
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 733)
 Fernandez, L., Komleu, C., Grimplet, J., Torregrosa, L. and Ageorges, A.
 Functional Genomics of Fruit Early Development in Grape (Vitis
 vinifera)
 Unpublished (2004)
 Contact: Ageorges A.
 Unite de Recherche des Produits de la Vigne
 Institut National de la Recherche Agronomique
 2, place Viala, 34 060 Montpellier Cedex 01, France
 Tel: 00-33-(0)4-99-61-27-56
 Fax: 00-33-(0)4-99-61-28-57
 Email: ageorges@ensam.inra.fr
 Seq primer: T7.
 Location/Qualifiers
 1..733
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Ugni Blanc"
 /db_xref="taxon:29760"
 /clone="3596 UB_S9_F11"
 /dev_stage="Green stage"
 /lab_host="DHS alpha"
 /clone_lib="wild type Ugni blanc SSH library"
 /note="Organ: Fruit; Vector: pgem-T; total RNA was
 isolated from 3, 6 and 15 days post anthesis for wild type
 and 'fleshless' mutated berries. cDNA was prepared from
 RNA (equal amount of the three developmental stages for
 each genotype) using the smart PCR cDNA system (Clontech).
 cDNA library was performed with the PCR-select cDNA
 subtraction kit (BD Biosciences, Clontech) using RNA from
 wild type as the tester and RNA from mutant as the
 driver."

ORIGIN
 Query Match 42.2%; Score 460, DB 8; Length 733;
 Best Local Similarity 79.0%; Pred. No. 1.3e-98;
 Matches 547; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 116 ATGCCCTTCACCTTCTGATGAGCAACGCCCATGCTTTTATGGGGGTAGATG 175
 |||||
 DB 692 ATGCCCTTACTGCTCTGAGTGAAGCTACACGCTAGTTTATGGGGGAGATG 633
 |||||

QY 176 CTTCAAGAACTATATGGGGAGAGCTTGTGGTATGGAAATCTGATGCACTGGTATGAA 235
 |||||
 DB 632 CCTTGGGACTATATGGAGAGGAGCTGTGTGATATGGAACTTGATCTCAGTGAATATGAG 573
 |||||
 QY 236 CTGAAGACTCAGCTTTAAGCACTGCTCTTATTTAATGATGAGCTTCTGTGCTAGTCT 295
 |||||
 DB 572 CAAGAAAGGAGCTTTGAGACAGAGCTTGTCAATATATGGGCTTCAATGTGGCAATGCT 513
 |||||
 QY 296 ACAAATTAATATGTGATTAACAATCAGCTTAGATGTGCATCAAGAGAAATCTGTAA 355
 |||||
 DB 512 ACAAGATCATATGTGATTAACAGATCCGATTCACAGTGTGCAAGAAAGAGCTTCTGTGA 453
 |||||
 QY 356 CCGTATATGCGCAAACTTTTGGCCCTCCCAATTTGGCCCTTCTTAACAATATGAGGCT 415
 |||||
 DB 452 CCAATCATGCAACAACTTTTGGCCCTCCCAACTATGCTCTTCCAAACAAATGAGAGGT 393
 |||||
 QY 416 GGTCAACCCCACTCAAGCAATTTGATATGAGCCCAACCGCTTGGAGAAAGATGTGA 475
 |||||
 DB 392 GGTCAACCCCACTCCGAGCACTTTTGAATATGAGTCAAGCAGATGGAGAAATGTGTA 333
 |||||
 QY 476 TTTACAGAGAGAGATGTCCCGTGTATTTTCAAGGGTTCCATGCAAAAGATGAG 535
 |||||
 DB 332 TTTACAGAGAGCGGAGATGTCCAGTGTGTCCAAAGGGTCCATGTAAGAGATGAG 273
 |||||
 QY 536 GGTATAGTTCACTGTGATATGAGAGAGTACTTTGAGCTAGTATGATCAGCAATGTG 595
 |||||
 DB 272 GTGTATGATTCAGTGTATATGAGAGAGTACTTCAATATGATATGATGATGATG 213
 |||||
 QY 596 GGGGTCTGATTCATTCATCAATGATGTTTCAATTAAGGCTCAAAACTGATGATGCGAA 655
 |||||
 DB 212 CTGGGCTGATTCATTCATCAATGATGTTTCAATCAAGGCTCCGAGCACTTGTATGCGCA 153
 |||||
 QY 656 TGTCAAGAAATGGGGTCTCAATTTGGCAATCCAAATGCGATTTGAATGGTCAATCTTTGT 715
 |||||
 DB 152 TGTTCAGAACTGGGAGCTAATGAGTGAAGAGTCAATATGCTAATGATGAGTCACTGTGT 93
 |||||
 QY 716 CCTTCAGGGTCAACCACTGATGAGAGACAGAGTTTCCAAGATATTTCCAGTAA 775
 |||||
 DB 92 CTTCAAGGTCAACCACTGATGAGTGAACCAAGATTCAGCAATGTTGTCTTCAG 33
 |||||
 QY 776 GTTGAATTCGGCCAACTTTCTTAGCCCA 807
 |||||
 DB 32 ATTGGGGTTTGTGTGACACCTTCTTAGCTCA 1
 |||||

RESULT 15
 AW704339 531 bp mRNA linear EST 14-JUL-2004
 LOCUS BK18B02.Y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1028-2500 5' similar to TR:Q39626 Q39626 EXPANSIN S2 PRECURSOR.
 !, mRNA sequence.
 ACCESSION AW704339
 VERSION AW704339.1 GI:7588483
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 531)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
 Schirck, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

QY 479 ACAGAGAGGAGATGTCCTCCGCTGCTATTTCAGAGGTTCCATGCAAAAAGCAT 531
DB 506 ACAGAGAGGAGATGTCCTCCGCTGCTATTTCAGAGGTTCCATGCAAAAAGCAT 558

RESULT 11
LOCUS CO100655 813 bp mRNA linear EST 16-JUN-2004
DEFINITION GR_Eb0026D10.r GR_Eb Gossypium raimondii cDNA clone GR_Eb0026D10
3', mRNA sequence.
ACCESSION CO100655
VERSION CO100655.1 GI:48799341
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 813)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
Global assembly of Cotton ESTs
TITLE Unpublished (2004)
JOURNAL Contact: Rod A. Wing
COMMENT Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu
Plate: 0026 row: D column: 10.
Location/Qualifiers
1. 813
FEATURES
source
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29720"
/clone="GR_Eb0026D10"
/issue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_Eb"
/note="Vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; library made by invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Query Match 42.9%; Score 466.8; DB 7; Length 813;
Best Local Similarity 77.7%; Pred. No. 3.3e-100;
Matches 564; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 47 AAAAAATGGCAAAATATGCTTTGGTACCTCATGATATGCTGTTCAAA 106
DB 87 AATTAATGGCAAAATATGCTTTGGTACCTCATGATATGCTGTTCAAA 146
QY 107 TCATCTACTATGCTTCACTTCGATGGAACCAAGCCCATGCTTTATAGGGG 166
DB 147 GCACCGTCAATGCTTCAAGGCTTCTGCTGATTAAGCTCAATTTATGAG 206
QY 167 GTATGATGCTTCAGAACTATAGGGGAGCTTGGGATAGGAAATCTGATGCACTG 226
DB 207 GCGGCAATGCTTCGGGAACATATGGGGAGCTTGGGATAGGAAATCTGATGCACTG 266
QY 227 GGTATGGAATCAAGACTGACGCTTTAAGCACTGCTTATTTATGATGAGCTTCTGTG 286
DB 267 GCTATGGAACAAGACTGCTGCTTTAAGTACTGCTTGTTCATTAATGAGACTTCATGTG 326
QY 287 GTATGCTCAAAATATATATGATATGATTAACAATGAGCTGATGATGATGCAAAAGAA 346
DB 327 GACAAATGCTATTAAGATATGATGATGATACAGACAGATCCAGATGGTGTCAATAAAGAA 386

QY 347 GATCTGTAACCGTAACTATGCGACAACCTTTTGGCCCTCCATTTTGGCCCTCTTAACACA 406
DB 387 CATCCGTAACCATTAACGACAACAACTTTTGTCTCTTAACCTTGTCTTCCAAACATG 446
QY 407 ATGAGAGCTGTGCAACCCACCACTCAAGCATTTTGTATATGAGCCCAACCCGCTTGGGAAA 466
DB 447 CCGAGAGCTGTGTAATCCACCCCTCAGACATTTGACATAGGCTCAGCCCTGGGAAA 506
QY 467 AGATTGATTTTACAGAGAGGAGATGTCCTCCGCTGCTATTTCAGAGGTTCCATGCAAAA 526
DB 507 AGATCGGTATCTACAGAGCGGAATGTGCCCCCTTTTGTTCAGAAAGGTTCTTGTCAAGA 566
QY 527 AGCATGAGAGGCTTATGATTCAGTGTGAATGGAGGAGCTACTTTAGCTGATATGATCA 586
DB 567 AGCATGTGAGAGGCTTACATCAATGAGAAAGCTATTTTCAGCTGTATGATTA 626
QY 587 GCATGTGAGGAGGCTGCTGATCCATCCATCAATGTTTCAATTAAGGCTCAAAAAGTGGAT 646
DB 627 GCATGTGTGTGCGCAGATCTATCCAGTCTGTGTCATCAAGGATCCAAAAGTGGGT 686
QY 647 GATGCAATGTCAAGAAATTTGGGTTCTTAATTTGGCAATCCAAATGCGTATTTGAATGTC 706
DB 687 GATGCAATGTCAAGAACTGGGAGCTTAATGCGCAATCCAAAGCTATCTCAATGCGC 746
QY 707 AATCTTTGCTTCACAGGCTACACCACTGATAGAGAGACAGATTTTCCAGATATG 766
DB 747 AATCATTTGCTTCAGGCTACACCACTGATGATGATGACTGACCAATTTCTGACATCG 806
QY 767 TTCCAG 772
DB 807 TGCTTG 812

RESULT 12
LOCUS CX017854/c 745 bp mRNA linear EST 07-DEC-2004
DEFINITION EST 1563 wild type Ugni blanc SSH library Vitis vinifera cDNA clone
3596 UB_S6_H01, mRNA sequence.
ACCESSION CX017854
VERSION CX017854.1 GI:56409602
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 745)
Fernandez,L., Romieu,C., Grimpel,J., Torregrasa,L. and Ageorges,A.
Functional Genomics of Fruit Early Development in Grape (Vitis
vinifera)
Unpublished (2004)
Contact: Ageorges A.
Unité de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-27-56
Fax: 00-33-(0)4-99-61-28-57
Email: ageorges@ensam.inra.fr
Seq primer: T7
FEATURES
source
1. 745
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultiivar="Ugni Blanc"
/db_xref="taxon:29760"
/clone="3596 UB_S6_H01"
/dev_stage="Green stage"
/lab_host="DH5 alpha"
/clone_lib="wild type Ugni blanc SSH library"
/note="Organ: Fruit; Vector: pGEM-T; Total RNA was
isolated from 3, 6 and 15 days post anthesis for wild type
and 'fleshless' mutated berries. cDNA was prepared from
RNA (equal amount of the three developmental stages for

digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the plasmid vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

ORIGIN

Query Match 46.0%; Score 501.4; DB 3; Length 533;
Best Local Similarity 99.8%; Pred. No. 1,6e-108;
Matches 502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      8  CTCACACCTCTCATTCATTAGGACATTCAGCAAGCAAGAAAAAATGCGCAAAATCATGCG 67
      31  TTTCACCTCTCATTCATTAGGACATTCAGCAAGCAAGAAAAAATGCGCAAAATCATGCG 90
QY      68  TTGTTTGGGTAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 127
      91  TTGTTTGGGTAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 150
QY      128  CTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 187
      151  CTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
QY      188  TGGGGGGAGGCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
      211  TGGGGGGAGGCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 270
QY      248  CTTTAAGCACTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
      271  CTTTAAGCACTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 330
QY      308  GTGATTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 367
      331  GTGATTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 390
QY      368  CAAACTTTTGCCCTCCCAATTTGCGCTTCTTCAACAACAATGAGGCTGTCACACCCAC 427
      391  CAAACTTTTGCCCTCCCAATTTGCGCTTCTTCAACAACAATGAGGCTGTCACACCCAC 450
QY      428  CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
      451  CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
QY      488  GGATCGTCCCGCTGCTATTTCGA 510
      511  GGATCGTCCCGCTGCTATTTCGA 533

```

RESULT 10
BE473899 558 bp mRNA linear EST 13-JUL-2004
LOCUS BE473899
DEFINITION Gm-c1043-2283 5' similar to TR:Q39626 Q39626 EXPANSION S2 PRECURSOR.
; mRNA sequence.

ACCESSION BE473899
VERSION BE473899.1 GI:9564390
KEYWORDS
SOURCE EST.
ORGANISM Glycine max (soybean)

REFERENCE 1 (bases 1 to 558)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Eipel, J., Coryell, V.,
Khamra, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
Boers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
Schurt, R., Ritter, E., Kohn, S., Shin, F., Jackson, Y., Cardenas, M.,
McCam, R., Waterston, R., and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)

COMMENT

Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1420 Std Error: 0.00
High quality sequence stop: 400.

FEATURES

source

Location/Qualifiers

1..558

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1043-2283"

/tissue_type="Hypocotyl and Plumule, germinating seeds"

/lab_host="DH10B"

/clone_lib="Gm-c1043"

/note="Vector: pT73Pac (Pharmacia), Site 1: EcoRI;

Site 2: NotI; This cDNA library was constructed from mRNA

isolated from hypocotyl and plumule tissues of seeds

germinated for three days of the cultivar Williams.

Complementary DNA was synthesized from mRNA using a primer

consisting of a poly(dT) sequence with a NotI restriction

site. EcoRI adapters were ligated to the blunt-ended cDNA

fragments followed by digestion with EcoRI and NotI. The

cDNA fragments were directionally cloned into the

EcoRI-NotI restriction site of the pT73-Pac vector. The

ligated cDNA fragments were transformed into DH10B host

cells (Gibco BRL). This library was constructed by Dr.

Randy Shoemaker."

ORIGIN

Query Match 43.5%; Score 473.6; DB 2; Length 558;
Best Local Similarity 94.6%; Pred. No. 7.4e-102;
Matches 504; Conservative 0; Mismatches 20; Indels 9; Gaps 1;

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QY      8  CTCACACCTCTCATTCATTAGGACATTCAGCAAGCAAGAAAAAATGCGCAAAATCATGCG 58
      26  TTTCACCTCTCATTCATTAGGACATTCAGCAAGCAAGAAAAAATGCGCAAAATCATGCG 85
QY      59  AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 118
      86  AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 145
QY      119  CTTTCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178
      146  CTTTCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 205
QY      179  CAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
      206  CAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
QY      239  GAACTGACCTTTAAGACATGCTTATTAATGATGATGATGATGATGATGATGATGATGAT 298
      266  GAACTGACCTTTAAGACATGCTTATTAATGATGATGATGATGATGATGATGATGATGAT 325
QY      299  AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
      326  AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 385
QY      359  TAACTGACCAAACTTTGCGCTTCCCAATTTGCGCTTCCCAATGATGATGATGATGATGAT 418
      386  TTAATGACCAAACTTTGCGCTTCCCAATTTGCGCTTCCCAATGATGATGATGATGATGAT 445
QY      419  GCAACCAACCACTCAAGATTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 478
      446  GCGAGCACCACCACTCAAGATTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 505

```

REFERENCE

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosida I; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 818)

AUTHORS

Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C., and Wang, R. A.

TITLE

Global assembly of Cotton ESTs

JOURNAL

Unpublished (2004)

COMMENT

Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 44 row: K column: 03.
Location/Qualifiers

FEATURES

source

1. 818
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Bb44K03"
/tissue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_1lb="GR_Bb"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; library made by Invitrogen with RNA supplied by Wendle lab. Directional clones into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Query Match 46.2%; Score 503.2; DB 7; Length 818;
Best Local Similarity 79.1%; Pred. No. 7e-109;

Matches 598; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

48 AAAAAAGGCAAAATCATCTGTTGGTGGAGGCTCATGGATTATGCTGTTACAAT 107
63 AGAATGGCAAAATCCATTTTGGATTACCAATTTCTGGATTATGCTATCGCTAC 122
108 CACTACTATGCTCTTCACCTCTGATGGAGGACCAAGCCCACTTTTATGGGG 167
123 TGATGTAAGTCCCTTCACGGCTTTGGGTGACCAAGACATGCTCATTTATGAGG 182
168 TAGTGATGCTTCAGGAATATGGGGGAGCTGTGGGATGGGAATCTGTATGCACTGG 227
183 CAGTGATGCTTCAGGAATATGGGGGAGCTGTGGGATGGGAATCTGTATGCACTGG 242
228 GTATGGAATGAACTGACAGCTTTAAGCACTGCTTATTTATGATGAGCTTCTGTGG 287
243 GTATGGAACAGGAGCTGCTCTTTAAGCAAGCTTGTTCATGATGAGCTTCATGTGG 302
288 TCAGTGCTACAAATATATATGATGATTACAATCAGATCAGATGAGTCAAGAGAG 347
303 ACAATGCTACAGATCGTGTGATTAACCTAGCTGACCTTAATGGGCAATAAAGGAC 362
348 ATCTGTAACGTAACCTGCAAACTTTTGGCCCTCCCAATTTCCGCTTCTAACAAC 407
363 ATCGTACACATCAACGCAAACTTTTGGCCCTCCCAATTTGCTTCCCAACATGC 422
408 TGAAGCTGCTGCAACCACTCAAGCAATTTGATATGAGCCCAACCGCTGGGAAA 467
423 CGAAGGTTGGTGCAACCTCTCTCCAGCACTTTGATATGAGCTCAGCTCGGGAAA 482
468 GATGTGATTTACAGAGAGGATCGTCCCGTCTATTTCAAGGGTTCATGCAAAA 527
483 GATGTGATTTACAGAGGATCGTCCCGTCTATTTCAAGGGTTCATGCAAAA 542
528 GCATGAGGGGTTAGTTCACTGATGATGGAGGAGCACTATTGAGCTAGTATGATCAG 587
543 ACATGAGGAGTACGTTCACTATCAACGAGAGAGCACTATTGAGCTAGTATGATCAG 602
588 CAATGTGGGGGTGCTGATTCATCAATCAGTGTCAATTAAAGGCTCAAAAAGCTGATG 647

Db

603 CATTGATGTTGGGCGAGATTCATTCATTCGATTCGTTAAAGGCTTAAATGGGTG 662

Qy

648 GATGCAATGTCAGAAATTTGGGTTCTTAATGGCAATCCATGCGTATTGAATGTC 707

Db

663 GATGCAATGTCAGAAATTTGGGTTCTTAATGGCAATCCATGCGTATTGAATGTC 722

Qy

708 ATCTTTGCTCTTCAGGTCACCACTATGATGAGAGACCAAGTTTCCAAATATGT 767

Db

723 ATGTTGTCGTTCAAGGTCAACCACTACCGATGATGTTACCCGACTGTTCCGATATGT 782

Qy

768 TCAGTATGTTGACATTTGGCCAACTTCTCTAG 803

Db

783 GCCTGCAAGTTGGGGGTTGGCCAGACTTCTCTAG 818

RESULT 9

BO079471

LOCUS

DEFINITION

BO079471 533 bp mRNA linear EST 05-JUL-2004
Ea14b09.y1 Gm-c1084 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1084-3905 5' similar to TR:Q39626 Q39626 EXPANSIN S2 PRECURSOR.
/, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

1 (bases 1 to 533)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Seepose, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco
High quality sequence stop: 383.

Location/Qualifiers

1. 533
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1084-3905"
/tissue_type="Bt isolated hypocotyls (Williams 82)"
/lab_host="Gm-c1084"
/clone_1lb="Gm-c1084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed by M. Bhattacharya
from mRNA isolated from etiolated hypocotyls from the
cultivar Williams 82. Tissue was inoculated with
Phytophthora sojae race 1 and tissues were harvested 2 and
4 hours following infection. The library is the pool of
these two time points. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI

QY 188 TGGGGGAGCTTGTGGGTATGGGAATCTGATGCACTGGGTATGGAAGTACAG 247
| | | | |
Db 197 TGGGGGAGCTTGTGGGTATGGGAATCTGATGCACTGGGTATGGAAGTACAG 256
| | | | |
QY 248 CTTTAAAGCACTGGCTTATTTAATGATGAGAGCTTCTGTGCTCAGTGTACAAAATTATAT 307
| | | | |
Db 257 CTTTAAAGCACTGGCTTATTTAATGATGAGAGCTTCTGTGCTCAGTGTACAAAATTATAT 316
| | | | |
QY 308 GTGATTAACAATGACACTGATGATGTCATCAAGAGAGATCTGATACCTGATACCGCA 367
| | | | |
Db 317 GTGATTAACAATGACACTGATGATGTCATCAAGAGAGATCTGATACCTGATACCGCA 376
| | | | |
QY 368 CAAACTTTGGCTCCCAATTTGGCCCTTCTTAACAACAATGAGAGGTGTGCAACCCAC 427
| | | | |
Db 377 CAAACTTTGGCTCCCAATTTGGCCCTTCTTAACAACAATGAGAGGTGTGCAACCCAC 436
| | | | |
QY 428 CACTCAAGCACTTTGATGATGAGCCCAACCCGCTTGGGAAAAGATTGATTTAAGAGAG 487
| | | | |
Db 437 CACTCAAGCACTTTGATGATGAGCCCAACCCGCTTGGGAAAAGATTGATTTAAGAGAG 496
| | | | |
QY 488 GATCGTCCCGTGTCTATTTCAAGAGGTTCATGCAAAAAGCATGAGAGGGTTAGGTTCA 547
| | | | |
Db 497 GATCGTCCCGTGTCTATTTCAAGAGGTTCATGCAAAAAGCATGAGATGCGTTAGGTTCA 556
| | | | |
QY 548 GTGTGAATGGAGGAGACTAC 567
| | | | |
Db 557 CTGTCAATGGGAGGAGACTAC 576
| | | | |

RESULT 7
BG585324 746 bp mRNA linear EST 11-APR-2001
LOCUS EST487088 MHAM Medicago truncatula/Gloms versiforme mixed EST
DEFINITION 1 library CDNA clone pMHAM-22F13 5' end, mRNA sequence.
ACCESSION BG585324 GI:13600388
VERSION BG585324.1
KEYWORDS EST.
SOURCE Medicago truncatula/Gloms versiforme mixed EST library
ORGANISM Medicago truncatula/Gloms versiforme mixed EST library
REFERENCE 1 (bases 1 to 746)
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.
and Frazer,C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
Gloms versiforme, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N380798e TIGR sequence name: MTDCC31TK More
information is available at: http://www.medicago.org
Seq primer: Skmod (CTA gaa cta gtc gat cc).
FEATURES
source
1..746
/organism="Medicago truncatula/Gloms versiforme mixed EST
library"
/mol_type="mRNA"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-22F13"
/tissue_type="roots colonized with Gloms versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Gloms versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="B. coli strain XLOLR"
/clone_id="MHAM"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; CDNA was prepared from polyA+ enriched RNA from

roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Gloms versiforme. The CDNA was
directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-aseist
helper phage and propagated in XLOLR cells."

ORIGIN
Query Match 47.8%; Score 520.8; DB 2; Length 746;
Best Local Similarity 83.6%; Pred.No.4,4e-113;
Matches 602; Conservative 0; Mismatches 117; Indels 1; Gaps 1;
QY 120 CTTCTACCTTCTGATGAGACCAAGCCCATGCTTTTATGAGGGGTAGTATGCTTC 179
| | | | |
Db 1 CTTCAAGCTTCTGATGAGACCAATGCTATGCACTTTTATGAGGGGTAGTATGCGGA 60
| | | | |
QY 180 AGGAACTATGGGGGAGCTTGTGGTATGGAATCTGTATGCACTGGGTAGAACTAG 229
| | | | |
Db 61 AGGCACTATGGGAGGAGCTTGTGGTATGGAATCTGTATGCAAGGGGTATGGAACAAG 120
| | | | |
QY 240 AACTGACGTTTATGACATGCTCTTATTTATGATGAGAGCTTCTGTGCTCAGTACGA 229
| | | | |
Db 121 AACGCTGCAATTAAAGTACTGCTTGTATATATGATGAGAGCTTCATGAGGCAATGCA 180
| | | | |
QY 300 AATTATATGATTAACAATCAGACTCTGATGATGATGATCAAGAAAGATCTGTAACCGT 359
| | | | |
Db 181 AATCATTTTGTATTAATGACAGACCAAGATGATGATTAAGAAAGATCTATACAT 240
| | | | |
QY 360 AACTGCAACAACTTTTGGCTCCCAATTTGCTTCCCTTAACAACAATGAGAGCTGAGT 419
| | | | |
Db 241 AACGCAACAAATTTTGTCTCTCAAAATTTTATCTTCCAAAGAGATGAGAGTGTG 300
| | | | |
QY 420 CAACCCACCACTCAGACATTTTATATGAGCCCAACCCGCTTGGGAAAAGATGATTTTA 479
| | | | |
Db 301 CAACCCACCTCTAAGACATTTTATATGAGCAACCTGCTTGGGAAAAGATGGAATCTA 360
| | | | |
QY 480 CAGAGAGAGGATGTCCCGTGTATTTCAAGAGGTTCCATGCAAAAAGATGAGAGGGT 539
| | | | |
Db 361 TAGAGAGAGGATGTCCCGTGTATTTCAAAAGGTTCTTGGCAAAAAGATGAGAGAGT 420
| | | | |
QY 540 TAGGTCAGTGTATGAGGAGGAGGACTTCTGATGATGATGATGATGATGATGATGATG 539
| | | | |
Db 421 TAGGTCAGTGTATGAGGAGGAGGACTTCTGATGATGATGATGATGATGATGATGATG 480
| | | | |
QY 600 TGCTGATCCATCCATCAGTGTCTTAAAGGCTCAAAAATCTGATGATGATGATGATG 659
| | | | |
Db 481 TGCTGATCCATCCATCAGTGTCTTAAAGGCTCAAAAATCTGATGATGATGATGATG 540
| | | | |
QY 660 AAGAAATGGGGTCTTAAATTTGCAATTCATGCGTATTTGATGATGATGATGATGATG 719
| | | | |
Db 541 AAGAAATGGGGTCTTAAATTTGCAATTCATGCGTATTTGATGATGATGATGATGATG 600
| | | | |
QY 720 CAGGTCACCAACCATGATGAGAGACCAAGTTTCCAAAGATGATGATGATGATGATG 778
| | | | |
Db 601 CAAAGTCACCAACCATGATGAGAGACCAAGTTTCCAAAGATGATGATGATGATGATG 660
| | | | |
QY 779 GGAATTTGGCCCAACTTCTTAGCCAGTTGATGATGATGATGATGATGATGATGATG 838
| | | | |
Db 661 GGAATTTGGCCCAACTTCTTAGCCAGTTGATGATGATGATGATGATGATGATGATG 720
| | | | |

RESULT 8
COL132031 818 bp mRNA linear EST 17-JUN-2004
LOCUS GR_Bb44K03.r GR_Bb Gossypium raimondii CDNA clone GR_Bb44K03.3',
DEFINITION mRNA sequence.
ACCESSION COL132031
VERSION COL132031.1 GI:48881009
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

source

1. 566
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl063-246"
/tissue_type="Hypocotyl and plumule, germinating seeds"
/lab_host="DH10B"
/note="Vector: pT73Pac (Pharmacia); Site 1: EcoRI; Site 2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestions with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

ORIGIN

Query Match 48.9%; Score 533; DB 2; Length 566;
Best Local Similarity 97.3%; Pred. No. 5.3e-116;
Matches 542; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 260 CCTTATTATGATGAGCTTCCGTGATGCTCAAAATATATGATTACAAAT 319
DB 10 CCGATTTATGATGAGCTTCTGTGTCAGTCTCAAAATATATGATTACAAAT 69
QY 320 CAGACTCTAGATGGTGCATCAAGAGATCTGTAACTGTACCCCAAACTTTTCC 379
DB 70 CAGACTCTAGATGGTGCATCAAGAGATCTGTAACTGTACCCCAAACTTTTCC 129
QY 380 CTCTCCAAATTTGCCCTTCTTAAACAATGAGGCTGTGACACCCCACTCAAGATT 439
DB 130 CTCTCCAAATTTGCCCTTCTTAAACAATGAGGCTGTGACACCCCACTCAAGATT 189
QY 440 TTGATATGAGCCCAACCGCTTGGGAAAGATGTTATTCAGAGGAGGATGTCCTCCG 499
DB 190 TTGATATGAGCCCAACCGCTTGGGAAAGATGTTATTCAGAGGAGGATGTCCTCCG 249
QY 500 TGTCTATTTCAAGGGTTCATGCAAAAGATGAGGGGTTAGGTTAGTGTGATGGA 559
DB 250 TGTCTATTTCAAGGGTTCATGCAAAAGATGAGGGGTTAGGTTAGTGTGATGGA 309
QY 560 GGGACTACTTGTGAGTGAATGATGCAATGTGGGGGGTGTGATCCATCCATCAG 619
DB 310 GGGACTACTTGTGAGTGAATGATGCAATGTGGGGGGTGTGATCCATCCATCAG 369
QY 620 TGTCTATTTAAAGGCTCAAAACCTGATGATGCAAGAAATTTGGGGTTCTAAT 679
DB 370 TGTCTATTTAAAGGCTCAAAACCTGATGATGCAAGAAATTTGGGGTTCTAAT 429
QY 680 GGGACTACTTGTGAGTGAATGATGCAATGTGGGGGGTGTGATCCATCCATCAG 739
DB 430 GGGACTACTTGTGAGTGAATGATGCAATGTGGGGGGTGTGATCCATCCATCAG 489
QY 740 GAGAGACGAGAGTTTTCAGAGATTTGTTCCAGTAAAGTGAATTTGGGCAAACTTCT 799
DB 490 GAGAGACGAGAGTTTTCAGAGATTTGTTCCAGTAAAGTGAATTTGGGCAAACTTCT 549
QY 800 CTGAGCCCAAGTTCAGTTC 816
DB 550 CTGAGCCCAAGTTCAGTTC 566

RESULT 6
Bg156427 576 bp mRNA linear EST 23-JUL-2004
LOCUS Bg156427
DEFINITION saa74f03.y1 Gm-cl063 Glycine max cDNA clone GENOME SYSTEMS CLONE

ACCESSION ID: Gm-cl063-246 5' similar to TR:Q39626 Q39626 EXPANSIN S2
PRECUSOR .; mRNA sequence.
Bg156427
VERSION Bg156427.1 GI:12690091
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max (soybean)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 576)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpellding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 394.
LOCATION/Qualifiers
1. 576
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl063-246"
/tissue_type="Germinating shoot, 24 hour germination"
/lab_host="DH10B"
/clone_1lb="Gm-cl063"
/note="Vector: pBluescript II SK-; Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to harvesting the germinating shoots. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

ORIGIN

Query Match 48.4%; Score 527.2; DB 2; Length 576;
Best Local Similarity 97.5%; Pred. No. 1.3e-114;
Matches 546; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 8 CTTCACCTCTCATCTATGAGTATGAGCAAGAGAAAAAATGGGCAAAATCATGC 67
DB 18 CTTCACCTCTCATCTATGAGTATGAGCAAGAGAAAAAATGGGCAAAATCATGC 76
QY 68 TTGTTTGGGTAGCCTCATTTGATTTGCTTTTCAAACTACTATGCTTTCTAC 127
DB 77 TTGTTTGGGTAGCCTCATTTGATTTGCTTTTCAAACTACTATGCTTTCTAC 136
QY 128 CTTCGTGATGAGCAACGCCCATGCACTTTTATGAGGGGTATGATGCTTCAGAACTA 187
DB 137 CTTCGTGATGAGCAACGCCCATGCACTTTTATGAGGGGTATGATGCTTCAGAACTA 196

Db 481 AATAAACAATCTTCAAGTTTAATTAAATTATACATTAATGTTGTAATATCATTTAA 540

QY 1059 GTTGAAGTTCAA 1070

Db 541 GTTGAAGTTCAA 552

RESULT 4

LOCUS BG352164

DEFINITION BG352164 541 bp mRNA linear EST 22-JUL-2004

PRECEDENCE ID: Gm-c1040-2859 5' similar to TR:Q39626 Q39626 EXPANSIN S2

ACCESSION BG352164

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 541)

AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritters, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 454.

FEATURES

Location/Qualifiers

1..541

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams 82"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1040-2859"

/tissue_type="Hypocotyl and Plumule, germinating seeds"

/lab_host="DH10B"

/note="Vector: PT73Pac (Pharmacia); Site 1: EcoRI; Site 2: NotI. This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestions with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the PT73-Pac vector. The ligated cDNA fragments were transformed into DH10 host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

ORIGIN

Query Match 49.1%; Score 535.2; DB 2; Length 541;

Best Local Similarity 99.4%; Pred. No. 1.6e-116;

Matches 537; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 CTCGATCATTTAGGATTCAGCAAGCAAGAAAAAATGGCAAAATCATGCTGTTT 74

Db 1 CTCGATCATTTAGGATTCAGCAAGCAATAAAAAAGGGCAAAATCATGCTGTTT 60

QY 75 GGTAGACCTCATTTGATTTAGCTGTTTCAAAATCACTATACCTTCACTTCTG 134

Db 61 GGTAGACCTCATTTGATTTAGCTGTTTCAAAATCACTATACCTTCACTTCTG 120

QY 135 ATGACCAAGCCCATGATCCATTTTATGAGGAGTATGATCTTCAGAACTATGAGGGG 194

Db 121 ATGACCAAGCCCATGATCCATTTTATGAGGAGTATGATCTTCAGAACTATGAGGGG 180

QY 195 AGCTTGGGATATGGAATCTGATGCACTGGGTATGAACTTGAACCTGACCTTTAG 254

Db 181 AGCTTGGGATATGGAATCTGATGCACTGGGTATGAACTTGAACCTGACCTTTAG 240

QY 255 CACTGCTTATTTAATGATGAGCTTCGTGGTCACTGCTCAAAATATATGATTA 314

Db 241 CACTGCTTATTTAATGATGAGCTTCGTGGTCACTGCTCAAAATATATGATTA 300

QY 315 CAATCAGACTAGATGATGATGATCAAGAAAGATCTGTAACCTGCAACAACTT 374

Db 301 CAATCAGACTAGATGATGATGATCAAGAAAGATCTGTAACCTGCAACAACTT 360

QY 375 TTGCTCTCCATTTGCTCTTCTTAACAACAATGAGGCTGTCACCCCACTTCA 434

Db 361 TTGCTCTCCATTTGCTCTTCTTAACAACAATGAGGCTGTCACCCCACTTCA 420

QY 435 GCATTTGATATGAGCCCAACCGCTTGGAAAAATTTGATTTACAGAGAGATCGT 494

Db 421 GCATTTGATATGAGCCCAACCGCTTGGAAAAATTTGATTTACAGAGAGATCGT 480

QY 495 CCCCCTGATTTCAAGAGGTTCCATGCAAAAGCATGAGAGGGGTTAGTTCACTGTA 554

Db 481 CCCCCTGATTTCAAGAGGTTCCATGCAAAAGCATGAGAGGGGTTAGTTCACTGTA 540

RESULT 5

LOCUS BG352954

DEFINITION BG352954 566 bp mRNA linear EST 22-JUL-2004

PRECEDENCE ID: Gm-c1040-2576 5' similar to TR:Q39626 Q39626 EXPANSIN S2

ACCESSION BG352954

VERSION BG352954

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 566)

AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritters, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 486.

FEATURES

Location/Qualifiers

Query Match 51.0%; Score 555.4; DB 3; Length 557;
Best Local Similarity 99.8%; Pred. No. 2,4e-121;
Matches 556; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 286 GGTCAAGTCTACAAATTTATGTGATTACAAATCAGACTCTAGATGGTCATCAAGGA 345
DB 1 GGTCAAGTCTACAAATTTATGTGATTACAAATCAGACTCTAGATGGTCATCAAGGA 60

QY 346 AGATCTGTAAACCGTAACTGTCACAACTTTTGCCCTCCAAATTTGCGCTTCTTAACAC 405
DB 61 AGATCTGTAAACCGTAACTGTCACAACTTTTGCCCTCCAAATTTGCGCTTCTTAACAC 120

QY 406 AATGAGAGGTGTGTGCAACCCACCACTAAGCATTTTATATGAGCCCAACCCGCTGGGAA 465
DB 121 AATGAGAGGTGTGTGCAACCCACCACTAAGCATTTTATATGAGCCCAACCCGCTGGGAA 180

QY 466 AAGATGTGTATTTAACAAGAGGAGTGTCCCGTGTATTTCAAAAGGTTCCATGCAAA 525
DB 181 AAGATGTGTATTTAACAAGAGGAGTGTCCCGTGTATTTCAAAAGGTTCCATGCAAA 240

QY 526 AAGCATGAGAGGGGTAGGTTCACTGTGTAATGGAAGGACTAATTGAGCTAGTATGATC 585
DB 241 AAGCATGAGAGGGGTAGGTTCACTGTGTAATGGAAGGACTAATTGAGCTAGTATGATC 300

QY 586 AGCAATGTGGGGGGTGTGATTCATCACTGTTCACTTAAAGGCTCAAAAACCTGGA 645
DB 301 AGCAATGTGGGGGGTGTGATTCATCACTGTTCACTTAAAGGCTCAAAAACCTGGA 360

QY 646 TGAATGGCAATGTCAAGAAATGGGGTTCATATTGGCAATCGCATGGTATTTGAATGAT 705
DB 361 TGAATGGCAATGTCAAGAAATGGGGTTCATATTGGCAATCGCATGGTATTTGAATGAT 420

QY 706 CAATCTTTTCTCTTCAAGGTCACCAACCACTGATGAGAGACAGAGTTTTCAGAGATAT 765
DB 421 CAATCTTTTCTCTTCAAGGTCACCAACCACTGATGAGAGACAGAGTTTTCAGAGATAT 480

QY 766 GTTCCAGTAAGTGTGACATTCGCGCAAACTTTCTTACGCCAGTTCACTTAAAGCTGAT 825
DB 481 GTTCCAGTAAGTGTGACATTCGCGCAAACTTTCTTACGCCAGTTCACTTAAAGCTGAT 540

QY 826 TACAGATTAACCAACCA 842
DB 541 TACAGATTAACCAACCA 557

RESULT 3
BM885693 559 bp mRNA linear EST 06-JUL-2004
LOCUS BM885693
DEFINITION Bam04a08.y1 Gm-cl063 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl063-4264 5' similar to TR:024208 024208 EXPANSIN PRECURSOR. ;
mRNA sequence.

ACCESSION BM885693
VERSION BM885693.1 GI:19269437
KEYWORDS EST.

SOURCE
ORGANISM Glycine max (soybean)
Glycine max

REFERENCE
AUTHORS Shoenaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schuck, R., Riteer, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCam, R., Waterston, R., and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Glibco
High quality sequence stop: 426.
Location/Qualifiers
1. 559
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl063-4264"
/issue_type="Germinating shoot, 24 hour germination"
/lab_host="DH10B"
/clone_11b="Gm-cl063"
/note="Vector: pBluescript II SK+; Site 1: EcoRI, Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from germinating shoots of the cultivar Williams. The
seeds were allowed to germinate for 24 hours prior to
harvesting the germinating shoots. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (Gibco BRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker at Iowa state university."

ORIGIN

Query Match 49.3%; Score 536.8; DB 3; Length 559;
Best Local Similarity 99.8%; Pred. No. 6.6e-117;
Matches 549; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 520 TGCAAAAGAGATGAGGGGTAGGTTCACTGTGTAATGGAAGGACTAATTGAGCTAGTA 579
DB 1 TGCAAAAGAGATGAGGGGTAGGTTCACTGTGTAATGGAAGGACTAATTGAGCTAGTA 60

QY 580 TTGATCAGCAATGTGGGGGGTGTGATTCATCACTGTTCACTTAAAGGCTCAAA 639
DB 61 TTGATCAGCAATGTGGGGGGTGTGATTCATCACTGTTCACTTAAAGGCTCAAA 120

QY 640 ACTGATGATGATGCAATGTCAAGAAATGGGGTTCATATTGGCAATCGCATGGTATTTGA 699
DB 121 ACTGATGATGATGCAATGTCAAGAAATGGGGTTCATATTGGCAATCGCATGGTATTTGA 180

QY 700 AATGATCAATCTTGTCTTCAAGGTCACCAACCACTGATGAGAGACAGAGTTTTCCAA 759
DB 181 AATGATCAATCTTGTCTTCAAGGTCACCAACCACTGATGAGAGACAGAGTTTTCCAA 240

QY 760 GATATTTTTCAGTAAGTGTGACATTCGCGCAAACTTTCTTACGCCAGTTCACTTAA 819
DB 241 GATATTTTTCAGTAAGTGTGACATTCGCGCAAACTTTCTTACGCCAGTTCACTTAA 300

QY 820 GCTGATTAACAATAACCAACCAAGGCTGAGGCGTCTTTTATTTATTTAGAGAC 879
DB 301 GCTGATTAACAATAACCAACCAAGGCTGAGGCGTCTTTTATTTATTTAGAGAC 360

QY 880 TGCCCGCACCTTCTTCTGTTGTTGATTTATTTCCCACTCAAGCCTCTATCAAG 939
DB 361 TGCCCGCACCTTCTTCTGTTGTTGATTTATTTCCCACTCAAGCCTCTATCAAG 420

QY 940 CATTAATTTTATCAATAAT-ACATCAATCACCATCATATCATTAAGCTGTATATC 998
DB 421 CATTAATTTTATCAATAAT-ACATCAATCACCATCATATCATTAAGCTGTATATC 480

QY 999 AATTAACATCTTCAAGTTAAATTAATTATTAATTAATTTGTTATATCATATATA 1058
DB 999 AATTAACATCTTCAAGTTAAATTAATTATTAATTAATTTGTTATATCATATATA 1058

/lab host="DH10B"
 /clone lib="Gm-cl046"
 /note="Vector: PT73Pac (pharmacia); Site 1: EcoRI;
 Site 2: NotI. This cDNA library was constructed from mRNA
 isolated from seeds germinated for three days of the
 cultivar Williams. Complementary DNA was synthesized from
 mRNA using a primer consisting of a poly(dT) sequence with
 a NotI restriction site. EcoRI adapters were ligated to
 the blunt-ended cDNA fragments followed by digestions
 with EcoRI and NotI. The cDNA fragments were
 directionally cloned into the EcoRI-NotI restriction site
 of the PT73-Pac vector. The ligated cDNA fragments were
 transformed into DH10B host cells (Gibco BRL). This
 library was constructed by Dr. Randy Shoemaker."

ORIGIN

Query Match 55.3%; Score 602.6; DB 2; Length 617;
 Best Local Similarity 98.5%; Pred. No. 1.4e-132;
 Matches 608; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

134 GATGACCAACGCCCATGCTTTTATGAGGGGTAGTGTCTCAAGAACTATGAGG 193
 1 GATGACCAACATGCGCCATGCTTTTATGAGGGGTAGTGTCTCAAGAACTATGAGG 60
 194 GAGCTTGTGGGTATGGAATCTGTATGCACTGGGTATGGAATGCACTGACGCTTAA 253
 61 GAGCTTGTGGGTATGGAATCTGTATGCACTGGGTATGGAATGCACTGACGCTTAA 120
 254 GCACTGCTTATTTATATGATGAGCTTCTGTGTGTCAGTCTCAAAAATATATGATT 313
 121 GCACTGCTTATTTATATGATGAGCTTCTGTGTGTCAGTCTCAAAAATATATGATT 180
 314 ACAATATGACCTAGATGTGTCATCAAGAAATCTGTAACCTGTAACCTGCAAACT 373
 181 ACAATATGACCTAGATGTGTCATCAAGAAATCTGTAACCTGTAACCTGCAAACT 240
 374 TTGGCCCTCCCAATTTGGCCCTTCTTAACAACATGAGGCTGTGCAACCCACTCA 433
 241 TTGGCCCTCCCAATTTGGCCCTTCTTAACAACATGAGGCTGTGCAACCCACTCA 300
 434 AGCATTTGATATGAGCCCAACCGCTTGGAAAAAGATTGATTTACAGAGAGGATCG 493
 301 AGCATTTGATATGAGCCCAACCGCTTGGAAAAAGATTGATTTACAGAGAGGATCG 360
 494 TCCCGCTGCTATTTCAAAAGGTTCCATGCAAAAAGCATGAGGCTTAAGTTCAATGTA 553
 361 TCCCGCTGCTATTTCAAAAGGTTCCATGCAAAAAGCATGAGGCTTAAGTTCAATGTA 420
 554 ATGGAGAGGACTACTTGTAGCTATGATCAGCAATGTGGGGGTGCTGATCCATCC 613
 421 ATGGAGAGGACTACTTGTAGCTATGATCAGCAATGTGGGGGTGCTGATCCATCC 480
 614 AATCAGTGTTCATTTAAAGGCTCAAAAATGAGATGAGCAATGTCAAAAATTTGGGTT 673
 481 AATCAGTGTTCATTTAAAGGCTCAAAAATGAGATGAGCAATGTCAAAAATTTGGGTT 540
 674 CTAAATGGCAATCCATGCGTATTTGATGATGCTCATCTTTGCTTCAAGGCTCAACCA 733
 541 CTAAATGGCAATCCATGCGTATTTGATGATGCTCATCTTTGCTTCAAGGCTCAACCA 600
 734 CTGATGAGAGAGACCAGA 750
 601 CTGATGAGAGAGACCAGA 617

RESULT 2
 BI699217
 LOCUS
 DEFINITION
 ID: Gm-cl081-526 5' similar to IR:Q39626 Q39626 EXPANSIN S2
 PRECURSOR. ; mRNA sequence.
 ACCESSION
 BI699217
 VERSION
 BI699217.1 GI:15661846

KEYWORDS

EST.
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eusterois I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

1 (bases 1 to 557)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
 Bowers, J., Peterson, B., Swallier, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Korn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Seq primer: -40RP from Gibco
 High quality sequence length: 421.

FEATURES

source

1. 557
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Brags"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl081-526"
 /tissue_type="Roots of 7 day old 'Brags' seedlings"
 /dev_stage="7 days old"
 /lab_host="DH10B"
 /clone_lib="Gm-cl081"
 /note="Vector: pBluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; The mRNA was isolated from roots of 7 day old
 'Brags' seedlings that were mock-infected 48 hours prior
 to harvest. Dr. Gary Stacey generously donated the
 tissue. The roots were flash-frozen in liquid nitrogen.
 StrataGene's cDNA Synthesis Kit (catalog number 200401)
 was used to synthesize the cDNA. First-strand synthesis
 was performed with 5-methyl dCTP, hence the ligated cDNA
 was hemimethylated. A modification of StrataGene's
 first-strand synthesis primer was used. An 'anchor'
 nucleotide (V=A, C, or G) was added to the 3' end of the
 primer [GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG(T)18V] to anchor
 the primer at the 5' end of the poly(A) tract. After
 second-strand synthesis, the cDNA ends were filled in with
 cloned pV DNA, ligated to EcoRI adapters and subsequently
 phosphorylated. The cDNA was then precipitated and
 redissolved in sterile, RNase-, DNase-free water. The XhoI
 site within the first-strand synthesis primer was then
 restricted by digestion with XhoI from Promega (40U/ul);
 all XhoI sites in the cDNA would be protected by their
 hemimethylated status. The cDNA constructs were
 size-fractionated with a 500bp cutoff, using Sephacryl
 S-500 High Resolution (Pharmacia Biotech) in a 2-mm
 diameter column and a bed volume of approximately 1ml. The
 column eluent was precipitated, redissolved, and ligated
 into StrataGene's pBluescript II XR Predigested vector
 (pBluescript II SK(+)) vector that has been digested with
 EcoRI and XhoI, and phosphorylated by StrataGene). This
 library was constructed in the laboratory of Dr. Paul Keim
 and Dr. Virginia H. Coryell at Northern Arizona
 University."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2006, 10:06:46 ; Search time 4303 Seconds
(without alignments)
11840.840 Million cell updates/sec

Title: US-10-660-499A-1

Perfect score: 1089

Sequence: 1 ggcagagctcaactctca.....aaaaaaaaaaaaaaaa 1089

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1_0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_g8a1.*
10: gb_g8a2.*
11: gb_g8a3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602.6	55.3	617	2	BE607657
2	555.4	51.0	557	2	BE607657
3	536.8	49.3	559	3	BE607657
4	535.2	49.1	541	2	BE607657
5	533	48.9	556	2	BE607657
6	527.2	48.4	576	2	BE607657
7	520.8	47.8	746	2	BE607657
8	503.2	46.2	818	7	BE607657
9	501.4	46.0	533	3	BE607657
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11	466.8	42.9	813	7	BE607657
12	463	42.5	745	8	BE607657
13	460	42.2	701	8	BE607657
14	460	42.2	733	8	BE607657
15	455.2	41.8	531	1	BE607657
16	452.2	41.5	798	6	BE607657
17	448.8	41.2	760	6	BE607657
18	446	41.0	808	6	BE607657
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23	426.6	39.2	775	6	CF208600
24	424.2	39.0	725	2	BE643838
25	423.6	38.9	630	6	CB915761
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27	421.2	38.7	790	5	BO505051
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29	421	38.7	918	7	CK288799
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34	412.6	37.9	737	8	DR912239
35	411.8	37.8	759	1	AJ794895
36	411.4	37.8	764	2	BG592929
37	411	37.7	768	8	CK017719
38	410.8	37.7	721	2	AJ560126
39	406	37.3	721	2	BJ126936
40	405.8	37.3	768	7	CV497500
41	402.6	37.0	666	2	BG588019
42	400.8	36.8	735	6	CF208736
43	399.6	36.7	418	2	BF009260
44	397.2	36.5	613	6	CB919975
45	396.8	36.4	610	6	CB919142

ALIGNMENTS

RESULT 1
BE607657
LOCUS
DEFINITION
BE607657 617 bp mRNA linear EST 13-JUL-2004
BGI507.Y1 Gm-c1046 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1046-901 5' similar to TR:Q3626 Q3626 EXPANSIN S2 PRECURSOR.
/, mRNA sequence.

ACCESSION
BE607657
VERSION
BE607657.1 GI:9898689
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
EST.
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
1 (bases 1 to 617)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, D.,
Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pope, D., Harvey, N.,
Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwaterston.wustl.edu

TITLE

JOURNAL

COMMENT
Public Soybean EST Project

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 858 Std Error: 0.00
High quality sequence stop: 451.
Location/Qualifiers

FEATURES

Source

1. 617
/organism="Glycine max"
/mol_type="mRNA"
/cultiivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1046-901"
/tissue_type="Germinating Seeds"

QY 768 TCACGAGTGGACATTCGCGCAACTTT 797
DB 1632 GCCTGCTGGTGGCAATCGACAAACTTT 1661

RESULT 15

US-08-298-687A-26
Sequence 26, Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
LIBRARY: EMBL-ST
CLONE: SIB12
US-08-298-687A-26

Query Match 13.3%; Score 145.2; DB 2; Length 2415;
Best Local Similarity 57.4%; Pred. No. 2.6e-29;
Matches 396; Conservative 0; Mismatches 208; Indels 86; Gaps 4;
QY 185 CTATGGGGAGCTTGTGGTATGGGAATCTGTATGCACTGGTATGAACTGAACTG 244
DB 981 CTATAGGGGAGCTGTGGTATGAAACCTGTACAGTCAAGGGTATGAAACGACGACAG 1040
QY 245 CAGCTTTAAGCACTGCTTATTATATGATGAGCTTCTGTGT-CACTGCTCAAAATT 303
DB 1041 CAGCTTTGAGCACTGCACTTTTCAACATGCTTGAAGCTGGGTCAGCTCTACGAGCTC 1100
QY 304 ATATGTGATTAACAATCAGACTAGATGTGTGATCAAGAAAGATCTGTACCGTAACT 363

DB 1101 CGGTG-----CAACATGATCTTCATGATGTCATTA--GTGCAACATAACCGTGACA 1151
QY 364 GGCAGAACTTTTGGCTCCCAATTTGCGCTTCCCAACAACAATGAGAGCTGTGCAAC 423
DB 1152 GGCACCAATTTTGTCCCTTACTATGCTTTATCTAGTACAAATGCGGGTGTCAAT 1211
QY 424 CCACCACTCAAGCATTTTGTATGATGCGCCCAACCGCTTGGGAAAAGATTGTATTTACAG 483
DB 1212 CCCCACAGAAACACTTTGATTTGGCCGACCGGATTTTGCAGATGCGGAAATTCGA 1271
QY 484 GGAGGATGTCCTCCGTCT-----ATTCAAGGGTTCATGCAAAA 503
DB 1272 GCTGGAATGTCCTGTTATGTTCAAGAGTGTGATTAACCTCAATTCAATCATCAC 1331
QY 504 -----ATTCAAGGGTTCATGCAAAA 527
DB 1332 ACTCTTAAAGTATGTTAACTGTGGGTGTTAACCTTTGCAAGGGTGTCAATGTGAA 1391
QY 528 GCATGAGGGGTTAGGTTCAAGTGTGAATGAGAGGACTATTGAGCTAGTATTCAG 587
DB 1392 GAAAGAGGCATCAGTTACCATGATGAGACATTGTACTTCAACATGTTGATTAAC 1451
QY 588 CAATGTGGGGGTGTGATTCATTCATCAGTTTCATTAAAGCTCAAAACTGGAAG 647
DB 1452 CAACGTGGAGGGGAGGGGATATAACGTCAAGTTCATCAAGTTCAAAAACAGAG 1511
QY 648 GATGGCAATGTCAAGAAATTTGGGGTTCTAATTGGCAATCCATGCGTATTTGAATGTC 707
DB 1512 GCTACTATGTCCAGAAATTTGGGCCAAACTGGGAGACAAATGCTTACTTAAACGCCA 1571
QY 708 ATCTTGTCTTCAGGGTCAACCACTGATGAGAGAGACAGAGTTTCCAGATATTTGT 767
DB 1572 AAGCTCTCTTTCAAAGTACATCGCAGCATGGCAGAGACTATACAACTACATGTAGT 1631
QY 768 TCACGTAAGTTGCACTTGGCCAAACTTT 797
DB 1632 GCCTGCTGGTGGCAATTCGACAAACTTT 1661

Search completed: January 11, 2006, 13:32:17
Job time : 244 secs

NAME/KEY: CDS
LOCATION: (1)..(501)
OTHER INFORMATION: strawberry expansin (FaeX1) partial cDNA clone
US-09-362-642-3

Query Match 16.7%; Score 181.4; DB 3; Length 501;
Best Local Similarity 61.4%; Pred. No. 1,9e-39;
Matches 309; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 181 GGAATATGAGGAGGAGCTTGTGGGTATGGAAATCTGTATGCAACTGGGTATGGAATGAGA 240
DB 1 GGAACCATGGGGGTGCTTGTGATATGAAACCTTACAGCAGGAGCTTACGGAGTCAAC 60
QY 241 ACTGACGCTTAAAGCACTGCTTATTTAATGATGAGACTTCTGTGTCTAGTGTACAA 300
DB 61 ACTGCTGCGCTGAGCAAGGCTGTGTTCAACAATGGCTGAGCTGCGCGCTTCTTCGAG 120
QY 301 ATTATATGTATTAACAATCAGACTAGATGATGATGATGATGATGATGATGATGATGATG 360
DB 121 ATCAATGTCGGGCAACCAACCAAGT--GGTGCATGCTCCGAAAGCCCTTCAATTTTCTC 177
QY 361 ACTGCAACAACTTTTGGCCCTCCCAATTTTGGCCCTTCTTAAACAATGAGGCTGTGTC 420
DB 178 ACCGCCACCAACTTCTGCGCTCCCAACTTCTGCTCAGCCGCAATGAGCGGTGTGTC 237
QY 421 AACCCACCACTCAAGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 238 AACCTTCCCGGAGCCCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 297
QY 481 AGAGAGGAGATGCTCCCGCTGCTATTTCAAAAGGCTTCATGCAAAAAGATGAGAGGGGT 540
DB 298 AAAGCGGAATGCTCCCGCTGCTTACCGCGGCTCCATGCTGAAGAGGGGTGATG 357
QY 541 AGGTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 358 AGGTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 601 GCTGATTCATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 418 GCAGGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
QY 661 AGAATTTGGGCTTCAATGAGCA 683
DB 478 CGAATTTGGGCTCAAACTGCA 500

RESULT 14
US-07-885-970A-26

Sequence 26, Application US/07885970A
Patent No. 5495070

GENERAL INFORMATION:

APPLICANT: John, Maliyakal B.

TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSER: Nicholas J. Seay, Quarles & Brady

STREET: P.O. Box 2113, First Wisconsin Plaza

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microbot Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/885,970A

FILING DATE: 19920518

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,239

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/253,243

FILING DATE: 04-OCT-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 283-2478

TELEFAX: (608) 251-5139

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 2415 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Gossypium barbadense

STRAIN: Sea Island

IMMEDIATE SOURCE:

LIBRARY: EMBL SI

CLONE: SIB12

US-07-885-970A-26

Query Match 13.3%; Score 145.2; DB 2; Length 2415;

Best Local Similarity 57.4%; Pred. No. 2,6e-29;

Matches 396; Conservative 0; Mismatches 208; Indels 86; Gaps 4;

QY 185 CTATGGGGGAGCTTGTGGGTATGGAATCTGTATGCAACTGGGTATGGAATGAGAACTG 244
DB 981 CTATAGGGGAGCTTGTGGGTATGGAATCTGTATGCAACTGGGTATGGAATGAGAACTG 1040
QY 245 CAGCTTAAAGCACTGCTTATTTAATGATGAGACTTCTGTGT--CAGTCTCAAAAT 303
DB 1041 CAGCTTAAAGCACTGCTTATTTAATGATGAGACTTCTGTGT--CAGTCTCAAAAT 1100
QY 304 ATATGTATTAACAATCAGACTTGTATGATGATGATGATGATGATGATGATGATGATG 363
DB 1101 CGGTG-----CAACAATGATCTCAATGATGATGATGATGATGATGATGATGATG 1151
QY 364 GCCACAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTT 423
DB 1152 GCCACAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTT 1211
QY 424 CCACCACTAAGCACTTTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 483
DB 1212 CCCCCAGAGAACCTTTGATATTTGATGATGATGATGATGATGATGATGATGATGATG 1271
QY 484 GAGGAGATGCTCCCGTGTCT-----ATTGCAAGGCTTCCATGCAAAA 503
DB 1272 GCTGGAATGCTCCCGTGTGTATGATGATGATGATGATGATGATGATGATGATGATG 1331
QY 504 -----ATTGCAAGGCTTCCATGCAAAA 527
DB 1332 ACTCTTAAAGTATGTTAAACTGTTGGTGTAACTTTTGGAGGCTTCAATGATGATG 1391
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DB 1392 GAAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1451
QY 588 CAATGAGGGGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 647
DB 1452 CAATGAGGGGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511
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US-08-787-335-5

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Best Local Similarity 63.8%; Pred. No. 5e-41;
Matches 284; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

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QY 413 GCTGTGACCAACCACTCAAGCATTTGATATGCGCCCAACCCGCTTGAGAAAAGATG 472
DB 62 GGTGTGACATCCCGACGAAACATTTGATTTGGCCGAACCGCAATCTTCCGATAG 121
QY 473 GTATTACAGAGAGATGTCCTCCGCTGCTATTTCAGAGAGATGCAATGCAAAAGCATG 532
DB 122 CAGAAATGCAAGCTGATGTCCTCTGTATGTCAGAGAGATGCTATGTTGAAGAG 181
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DB 182 GAGGCAATGAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
QY 593 TGGGGGGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 652
DB 242 TGGAGGGGCGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 301
QY 653 CAATGTCAAAATTTGGGGTTCTAATTTGCAATGCAATGCAATGCAATGCAATGCAAT 712
DB 302 CTATGTCAAAATTTGGGGTTCTAATTTGCAATGCAATGCAATGCAATGCAATGCAAT 361
QY 713 TGTCTTCAAGGTCACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 772
DB 362 TCTCTTTTAAAGTACCTGACGATGATGATGATGATGATGATGATGATGATGATGAT 421
QY 773 TAAATTGACATTTGCGCAAACTTT 797
DB 422 CTGTTTGGCAATTCGACAAACTTT 446

RESULT 12
US-08-845-539-3
Sequence 3, Application US/08845539
Patent No. 592303

GENERAL INFORMATION:

APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 1..501
OTHER INFORMATION: /product="strawberry FaEx1"

US-08-845-539-3

Query Match 16.7%; Score 181.4; DB 2; Length 501;
Best Local Similarity 61.4%; Pred. No. 1.9e-39;
Matches 309; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 181 GGAATCTATGGGGAGCTTGTGGGATATGGAATCTGTATGCAACTGGATGAACTAGA 240
DB 1 GGAACATGAGGGGGTCTGTGATATGGAACCTTACAGCCAGGCTAAGAGTCAAC 60
QY 241 ACTGCACTTTAAGCACTGCTTATTTAATGATGAGCTTCTGTGATGATGATGATGATG 300
DB 61 ACTGCTGCTGAGCAAGCTCTGTTCAACATGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120
QY 301 ATTATATGATTTAACAATCAACTGATGATGATGATGATGATGATGATGATGATGATG 360
DB 121 ATCAATGCGGCGAGCAAGCCAAAGT---GATGCACTGCGGAAAGCCCTTCATTTTCGTC 177
QY 361 ACTGCAACAATTTTGGCTTCCCAATTTGCGCTTCTTAACAAGATGAGGCTGATG 420
DB 178 ACCGCAACAATTTGCGCTTCCCAATTTGCTGCAAGCCAGCAAGATGAGGCTGATG 237
QY 421 AACCCCACTCAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 238 AACCTTCCCGAGCCCACTTGAACCTTGGCAAGCTTGTCAAGATGCGGATGATG 297
QY 481 AGAGAGGATGCTCCCGTCTATTTCAAGGTTCAATGCAAAAGATGAGGATG 540
DB 298 AAGCCGATGATGCTCCCGTCTATTTCAAGGTTCAATGCAAAAGATGAGGATG 357
QY 541 AGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 358 AGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 601 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 418 GCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
QY 661 AGAATTTGGGGTTCTAATTGCA 683
DB 478 CGAATTTGGGGTTCAAACTGCA 500

RESULT 13
US-09-362-642-3
Sequence 3, Application US/09362642
Patent No. 6350935

GENERAL INFORMATION:

APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 501
TYPE: DNA
ORGANISM: Fragaria x ananassa
FEATURE:

```

1 GENERAL INFORMATION:
2 APPLICANT: John, Maliyekal E.
3 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
4 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
5 NUMBER OF SEQUENCES: 33
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Nicholas J. Seay, Charles & Brady
8 STREET: P. O. Box 2113, First Wisconsin Plaza
9 CITY: Madison
10 STATE: Wisconsin
11 COUNTRY: USA
12 ZIP: 53701
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Microsoft Word
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/298,829
21 FILING DATE: 19-OCT-1994
22 CLASSIFICATION: 800
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 07/885,970
25 FILING DATE: 18-MAY-1992
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/617,239
28 FILING DATE: 21-NOV-1990
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 07/253,243
31 FILING DATE: 04-OCT-1988
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Seay, Nicholas J.
34 REGISTRATION NUMBER: 27,386
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (608) 283-2478
37 TELEFAX: (608) 251-5139
38 INFORMATION FOR SEQ ID NO: 6:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 727 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: double
43 TOPOLOGY: linear
44 MOLECULE TYPE: cDNA
45 HYPOTHETICAL: NO
46 ANTI-SENSE: NO
47 ORIGINAL SOURCE:
48 ORGANISM: Gossypium hirsutum
49 STRAIN: Coker 312
50 DEVELOPMENTAL STAGE: 10 day old fiber cells
51 TISSUE TYPE: fiber cells
52 IMMEDIATE SOURCE:
53 LIBRARY: CKEB10
54 CLONE: B12
55
56 US-08-298-829-6

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Accession	Sequence	Position
Db	GAGGCACTCAGTATGACACCAAGAAATGACATCTTGTAATCAATGATGGATGTGTGTAATGCAAGC	242
Oy	TGGGGGGGTCTGGATTCATTCCAATCAGGTTCATTAAAGGCTCAAAAATTGATGATGAG	655
Db	TGGAGAGGGCAGGGGATATATACGTACGTGTCCATAGAGGTTCCAGAACGAGATGGCTAC	301
Oy	CAATGTCAGAAATTGGGGTTCCTAATTGGCAATCCAAATGCTAATTTGATGATGTCATCTT	712
Db	CTATGTGTCAGAAATTGGGGCTCAAACTGGCAGAGCAATGCTTACCTTAAACGACAAAGCC	361
Oy	TGTCCTTCAGGGTCACACCACTGATGAGAGAACAGAGTTTCCAAATATTTGTTCAG	772
Db	TCTCTTTTAAAGTATGTCACAGCGATGCGACGAGCTATCAACAGCTTACAAATGTATGTGCTTG	421
Oy	TAAGTTGACATTCGGGCAAACTTT	797
Db	CTGGTTGGCAATTCGACAAACTTT	446

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? HYPOTHETICAL: NO
 ? ANTI-SENSE: NO
 ? ORIGINAL SOURCE:
 ? ORGANISM: *Gossypium hirsutum*
 ? STRAIN: Coker 312
 ? DEVELOPMENTAL STAGE: 10 day old fiber cells
 ? TISSUE TYPE: fiber cells
 ? IMMEDIATE SOURCE:
 ? LIBRARY: CKF810
 ? CLONE: B12
 ?
 ?
 US-08-298-687A-6

Query Match	17.2%;	Score 187.4;	DB 2;	Length 727;
Best Local Similarity	63.8%;	Pred. No. 5e-41;		
Matches 284;	Conservative 0;	Mismatches 161;	Indels 0;	Gaps 0;

OY		353	TAAACGTAATCTGCACAAAATTTCGGCCCTCCCAATTTGGCCCTTCTCATAACAAGATGGAG	4112
Dd		2	TAAACGTGAACAGCACMAACTTTTGCCAACCTAATGATGCTTATCTAATGACAATGGCG	61
OY		413	GCTGTGTCACACCACCACTCAAGCATTTTGATATGGCCCCAACCCCCTGTGGAAAAAATTTG	4727
Dd		62	GGTGTGTGCATATCCCCACAGAAACACTTTGATTTTGGCCGAACCGGCAATCTTCGGATAG	121
OY		473	GTAATTACAGAGAGGGATCGTCCCGCTGATTTTCAAAGGTTTCATGCAAAAGCATG	5322
Dd		122	CAGAATATACGTGAGCTGAAATCGTCCCTGTTATATGTTACAAAGGGTGTCAATGTGTGAAGAAAG	1811
OY		533	GAGGGATTAGGTTTCACTGTGAATGGAGGAGACTACTTTGAGCTAGTATTTGATCAGCAATG	5922
Dd		182	GAGGCATCAGGTAACACATGAATAGCAATTCGTACTTCAACATGATGTTGATPAACGAACG	2411
OY		593	TGGGGGTGCTGTGATCCATCCATCACTAGTGTTCATTAAAGCTCTAAAAAATCGATGATGG	6532
Dd		242	TGGGAGGGGCAGGGGATATPACGTCACTGTGCCATCAAGGGTTTCAGAAACGGAATGGCTAC	3011
OY		653	CAATGTCAGAAATTGGGGTTCTTAATTGGCAATCCATGGGTATTTGAATGGTCAATCTT	7121
Dd		302	CTATGTCCAGAAATTTGGGCCCCAAAACCTGGCAGAGCAATGCTTACCTTTAACGCAAAAGCC	3611
OY		713	TGTCTTCAAGGTCACCAACACTGATGAGAGACCAAGATTTTTCAAGATATTTGTTCCAG	7727
Dd		362	TCTCTTTTAAAGTAGCTGCGACGAGATGGCAGACACTATCAAGACCTCAATATGATGCTGTG	4211
OY		773	TAAATTGACATTTGGGCCAAACTTT	797
Dd		422	CTGGTTGGCAATTTGGCAAACTTT	446

RESULT 9
US-08-530-797-5
Sequence 5, Application US/08530797
Patent No. 5597718
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
APPLICANT: Umbeck, Paul F.
APPLICANT: Brill, Winston J.
TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
TITLE OF INVENTION: FOR ALTERED FIBER
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Quarles and Brady
STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/530,797
3 FILING DATE: 20-SEP-1995
4 CLASSIFICATION: 800
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 07/617,239
7 FILING DATE: 21-NOV-90
8 APPLICATION NUMBER: US 07/253,243
9 FILING DATE: 04-OCT-88
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Nicholas J. Seay
12 REGISTRATION NUMBER: 27,386
13 REFERENCE/DOCKET NUMBER: 112299024E
14 INFORMATION FOR SEQ ID NO: 5:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 727 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULAR TYPE: cDNA to mRNA
21 HYPOTHEetical: no
22 ANTI-SENSE: no
23 ORIGINAL SOURCE:
24 ORGANISM: Gossypium hirsutum
25 STRAIN: Coker 312
26 DEVELOPMENTAL STAGE: 10 day old fibro
27 TISSUE TYPE: fiber cells
28 IMMEDIATE SOURCE:
29 LIBRARY: CKP810
30 CLONE: B12
31
32 US-08-530-797-5

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Query Match	17.2%;	Score 187.4;	DB 2;	Length 727;
Best Local Similarity	63.8%;	Pred. No. 5e-41;		
Matches 284;	Conservative	0;	Mismatches 161;	Indels 0;
			Gaps	0;

QY	353	TAACCGTAACGTGCACAAACCTTTTGCCCTCCCAATTTCCGCTTCTTAACACAAATGGAG	4112
Db	2	TAACCGTACAGCCACCAACTTTTGTCCACTTACATGCTTTATCTAGTGAACAAATGGCG	61
QY	413	GCTGGTGCACCCCACTCAAGCATTTTGTATATGGCCCAACCCGCTTGGAAAAAGATTG	4722
Db	62	GGTGGTGCATCTCCCAACAGAAACTTTGATTTGGCCCAACCGGCAATCTTGCGGATAG	1211
QY	473	GTATTTACAGAGGAGGAGATGTCGCCCGTCTATTTCCAAAGGGTTCCATGCACAAACCATG	5322
Db	122	CAGAAATATCGACCTGGAAATGTCCTCTGTATATGTTCAAGAGGGTGTATGTGTGAAGAAAG	1811
QY	533	GAGGGGTTAGTTCTAGTGTGAATGGGAGGAGCTACTTTGAGCTAGTATTGATCAGCAATG	5922
Db	182	GAGGCATACGTATACACAAATGATATGACATTCGTACTTCAACATGATGTTGATTAACGAACG	2411
QY	593	TGGGGGGGTCTGGATTCATCCATCACTGTTCTATTAAAGGCTCAAAAACTGATGTGATGG	6522
Db	242	TGGGAGGGGCAGGGGATATATACGTACATGTCATCAAGGGTTTCCAAACCGAATGGCTAC	3011
QY	653	CAATGTCAAGAAATTTGGGGTTCTAATTTGGCAATCCAATGCGTATTTGAATGTGCAATCTT	7122
Db	302	CTATGTCCAGAAATTTGGGGCCAAACCTGCACAGACATGTCTTACCTTAACGACCAAAAGCC	3611
QY	713	TGTCTTCAAGGTCACACCACTGATGAGAGACCAAGATTTTCCAAGATATTTGTTCCAG	7722
Db	362	TCTCTTTTAAAGTGAATGCTGCACAGATGGCAGAGACTATCACAGGCTCAATGTATGTGCTTG	4211
QY	773	TAAATTTGACATTTGGGCCAAACTTT	797
Db	422	CTGGTTTGGCAATTCGACAAACTTT	446

RESULT 10
US-08-298-829-6
; Sequence 6, Application US/08298829
; Patent No. 5620882

QY 566 ACTTGAGCTAGTATGATGAGCAATGTGGGGGGTCTGATCCATCCAAATGAGTTCA 625
 Db 419 ACTTCATTTGGTGTATATCAACCACTCGGGGTGCAAGGAGATATGTCAGGGTCAAGC 478
 QY 626 TTAAGGCTCAAAACATGAGTATGAGTCAATGTCAAGAAATTTGGGGTTTAAATTGGCA 683
 Db 479 TAAAGGATCAACACCGGTTGATGAGCAATGACTGTAATTTGGGGCCAAACTGGCA 536

RESULT 7
 US-07-885-970A-6

; Sequence 6, Application US/07885970A
 ; Patent No. 5495070
 ; GENERAL INFORMATION:
 ; APPLICANT: John, Malyakal E.
 ; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: USA
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/885,970A
 ; FILING DATE: 19920518
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/617,239
 ; FILING DATE: 21-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/253,243
 ; FILING DATE: 04-OCT-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27,386
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 283-2478
 ; TELEFAX: (608) 251-5139
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 727 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Gossypium hirsutum
 ; STRAIN: Coker 312
 ; DEVELOPMENTAL STAGE: 10 day old fiber cells
 ; TISSUE TYPE: fiber cells
 ; IMMEDIATE SOURCE:
 ; LIBRARY: CKFB10
 ; CLONE: B12
 ; US-07-885-970A-6

Query Match 17.2%; Score 187.4; DB 2; Length 727;
 Best Local Similarity 63.8%; Pred. No. 5e-41;
 Matches 284; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 353 TAAACGTAAGTCCGACAACTTTGGCCCTCCCATTTGCGCCTTCCCAACAAGAGAG 412
 Db 2 TAAACGTAAGCAGCACCAACTTTGTCCACTAACTAAGCTTATCTAGTGAACATGCG 61

QY 413 GCTGTGCAACCAACCACTCAAGCATTTGTATATGAGCCCAACCCGCTTGGGAAAAGATG 472
 Db 62 GTGTGTGCAATCCCCCAGAAACATTTGATTTGGCCGACGCAATCTTTCGGATAG 121
 QY 473 GATATTACAGAGAGGATGTCCTCCGTCCTATTTCAAAGGTTCCATGCAAAAAGCATG 532
 Db 122 CAGATATTCAGAGCTGGAATGTCTCTTTATGTTCAGAGGGGTGTAATGTGAAGAAG 181
 QY 533 GAGGGGTTAGTTCACTGTGAATGAGAGGACTATTGAGTATGATATGATGACATG 592
 Db 182 GAGGCATCAGTACACCATGAATGACATTCGTAATCTCAACATGATGTGATACGAACG 241
 QY 593 TGGGGGGTCTGATCATCATCATCTGTTCTATTAAAGCTCAAAAACGTGATGATG 652
 Db 242 TGGAGGGGAGGAGGATATTAACGTCATCAAGGGTTCCAGAACAGATGCTAC 301
 QY 653 CAATGTCAAGAAATTTGGGGTTCTAATTGGCAATTCATGCGTATTTGATGATGCAATCTT 712
 Db 302 CTATGTCAGAAATTTGGGGCCAAACTGCGAGCAATGCTTACCTTAACGACAAAGCC 361
 QY 713 TGTCTTCAGGGTACCAACCACTGATGAGAGACCAAGATTTTCAAGATATTTGTCAG 772
 Db 362 TCTCTTTAAAGTACTGCGAGGATGGCAGACTATCACAGCCTCAATGTAGTGCTG 421
 QY 773 TAACTGACATTCGCGCAACTTT 797
 Db 422 CTGTTGCAATTCGACAAACTTT 446

RESULT 8

US-08-298-687A-6
 ; Sequence 6, Application US/08298687A
 ; Patent No. 5521078
 ; GENERAL INFORMATION:

; APPLICANT: John, Malyakal E.
 ; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: USA
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/298,687A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/617,239
 ; FILING DATE: 21-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/253,243
 ; FILING DATE: 04-OCT-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27,386
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 283-2478
 ; TELEFAX: (608) 251-5139
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 727 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA

NAME/KEY: CDS
LOCATION: (28):(702)
OTHER INFORMATION: tomato expansin (LeEx1)
US-09-362-642-1

Query Match 19.7%; Score 216.6; DB 3; Length 702;
Best Local Similarity 60.7%; Pred. No. 5.5e-49;
Matches 390; Conservative 0; Mismatches 249; Indels 4; Gaps 2;

72 TTTGGTAGCCTGATGATTAATGCTGTTTCAATCACTACCT-ATGCTCTCACTT 130
59 TTTTGTAGCTGATGTTTCAATGTTTGAAGAAATCCGTGGTGTACTCTGGTG 118
131 CTGATGAGCAACGCCCATGCACTTTTATGAGGGTATGATGCTTCAAGAACTATG 190
119 GTTCATGAGGAACCTGCAATGCTACATTTTACCGGAACTGATGCTTCTGGAACATG 178
191 GGGGAGCTGTGGGTATGGAATCTGATGCAACCTGGATGAGCTGAGCACTT 250
179 GCGGTGCTGTGTGTTATGAAATTTTACGCCAAGATAGGAGTTACACAGCAGC 238
251 TAAGACCTGCTTATTTAATGATGAGCTTCTGTGTCAGTCTCAAAATTTATATG 310
239 TAGTACTGCTTTGTTTAAATGATTAAGTTGAGAGCTGTTTGAATTAATGTA 298
311 ATTACAAATCACTCTAGATGCTCAAGAAAGATGTAACCGTA--ACTGCCA 367
299 CAATATCTCTAATGGAATGCTGCTTCTCGAAACCTTCATTTTATCAACAGCTA 358
368 CAACTTTTGGCCCTCCCAATTTGCGCTTCTAACAACATGAGGCTGTGCAACCC 427
359 CCAATTTTGGCCCAACAAATTAAGCTGTGCAATGCAATGAGTGTGTTACCCCTC 418
428 CACTCAAGACTTTTGAATGATGCAACCCGCTTGGGAAAGATGATTTATCAAGAG 487
419 CTGCGCTCACTTTGACCTGCTATGCTATGTTTCTCAAACTTGTCTAGTACCGGCTG 478
488 GGAATGCTCCCGTCTAATTTCAAGGCTTCATGCAAAAGATGAGAGGGGTATGCTCA 547
479 GCAATGCTCTTACTGATTAATGCAAGATCCATGCGAAAGCAAGAGATCAAGATTA 538
548 GTGTGATGAGGAGGACTCTTGAAGTATGATGATGAGCAATGAGGGGTGCTGAT 607
539 CCAATCAATGATTCCTGTTACTTAAGTATGATGATGATGAGGAGGCTGAG 598
608 CCAATCAATGATGATTAAGGCTCAAAAGCTGATGATGATGATGATGATGATGAT 667
599 ATATTATTAAGTTTGGGTAAAGAAAGAAAGAAAGAAATGATGATGATGATGATGAT 658
668 GGGGTTCTAATTTGCAATCAATGCTATTTGAATGCTCAATC 710
659 GGGGCAAAATTTGCAATCAATGCGGTTTAACTGCTCAATC 701

RESULT 4
US-08-845-539-1
Sequence 1, Application US/08845539
Patent No. 5929303

GENERAL INFORMATION:

APPLICANT: Bennet, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 28..702
OTHER INFORMATION: /product= "tomato LeEx1"

Query Match 19.7%; Score 215; DB 2; Length 702;
Best Local Similarity 60.5%; Pred. No. 1.5e-48;
Matches 389; Conservative 0; Mismatches 250; Indels 4; Gaps 2;

72 TTTGGTAGCCTGATGATTAATGCTGTTTCAATCACTACCT-ATGCTCTCACTT 130
59 TTTTGTAGCTGATGTTTCAATGTTTGAAGAAATCCGTGGTGTACTCTGGTG 118
131 CTGATGAGCAACGCCCATGCACTTTTATGAGGGTATGATGCTTCAAGAACTATG 190
119 GTTCATGAGGAACCTGCAATGCTACATTTTACGGGAAAGATGCTTCTGAAACATG 178
191 GGGGAGCTGTGGGTATGGAATCTGATGCAACCTGGATGAGAACTAGAACCTGCACTT 250
179 GCGGTGCTGTGTGTTATGAAATTTATACGCCAAGATAGCGAGTTACACAGCAGC 238
251 TAAGACCTGCTTATTTAATGATGAGCTTCTGTGTCAGTCTCAAAATTTATATG 310
239 TAGTACTGCTTTGTTTAAATGATTAAGTTGAGAGCTGTTTGAATTAATGTA 298
311 ATTACAAATCACTCTAGATGCTCAAGAAAGATGTAACCGTA--ACTGCCA 367
299 CAATATCTCTAATGGAATGCTGCTTCTCGAAACCTTCATTTTATCAACAGCTA 358
368 CAACTTTTGGCCCTCCCAATTTGCGCTTCTAACAACATGAGGCTGTGCAACCCAC 427
359 CCAATTTTGGCCCAACAAATTAAGCTGTGCAATGCAATGAGTGTGCTGTATACCCCTC 418
428 CACTCAAGACTTTTGAATGATGCAACCCGCTTGGGAAAGATGATTTATCAAGAGAG 487
419 CTGCGCTCACTTTGACCTGCTATGCTATGCTTCTCAAACTGCTCAGTACCGGCTG 478
488 GGAATGCTCCCGTCTAATTTCAAGGCTTCATGCAAAAGATGAGAGGGGTATGCTTCA 547
479 GCAATGCTCTTACTGATTAATGCAAGATCCATGCGAAAGCAAGAGAAATCAAGATTA 538
548 GTGTGATGAGGAGGACTCTTGAAGTATGATGATGATGATGAGGGGTGCTGAT 607
539 CCAATCAATGATTCCTGTTACTTAAGTATGATGATGATGATGATGATGATGAT 598
608 CCAATCAATGATGATTAAGGCTCAAAAGCTGATGATGATGATGATGATGATGAT 667
599 ATATTATTAAGTTTGGGTAAAGAAAGAAAGAAAGAAATGATGATGATGATGATGAT 658
668 GGGGTTCTAATTTGCAATCAATGCTATTTGAATGCTCAATC 710

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QY 252 AAGCACTGCTTATTTATGATGAGCTTCTGTGTCAGTGTCAAAAATTATATGTA 311
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QY 312 TTACAATGAGACTCTAGATGTGTGATCAAAAGAGATCTGTAACTGCACTGCA 371
    187 ----ACAAAGAGACCTTAATATGTGTGCTTCCGGGA---CTATTAGGGTCACTCCACAA 239
QY 372 CTTTGGCCCTCCCAATTTGGCCCTTCTTAACAACAATGAGGCTGGTCAACCACT 431
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Db 240 CTTTGGCCCTCCCAATTTGGCTCTCTTAACAACAATGAGGCTGGTCAACCACT 299
QY 432 CAAGCATTTTGAATATGAGCCCAACCGCTTGGGAAAAGATTGTATTTACAGAGAGG 491
    300 CCAACACTTGACATGAGCTGAGCTGCTCTTCAATGCTCAATACCAAGCTGTAT 359
QY 492 CGTCCCGTGTCTATTTCAAAGGCTCCATGCAAAAAGCATGAGGAGTTAGTTCA 551
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Db 360 CGTCCCGTGTCTATTTCGATGAGGATCAATGATGAAGAAAGGTGAGTGAATTA 419
QY 552 GAAATGAGGAGCTACTTGTAGCTAGTATGATCAGCAATGTGGGGGTCTGATCAT 611
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QY 672 TTCTAATGAGCAATCCAAATCGTATTTGAATGTGCAATCTTGTCTTCAAGG 731
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Db 540 CCAAACTGCAAGAGCAACAATCTATCTCAATGCGCAAGGCTTCTTCAAGTCA 599
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Db 660 AACCTATGAAGGCC 674
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RESULT 2
US-09-092-160-1
; Sequence 1, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullitman, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092.160C
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440.517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242.090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060.944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
; OTHER INFORMATION: expansin
US-09-092-160-1

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Query Match 25.6%; Score 278.6; DB 3; Length 681;
Best Local Similarity 65.5%; Pred. No. 7.1e-66;
Matches 442; Conservative 0; Mismatches 224; Indels 9; Gaps 2;

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QY 192 GGGAGCTTGGGATATGAGAACTGTATGCACTGAGTATGGAATCTAGAACTGCACT 251
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QY 252 AAGCACTGCTTATTTATGATGAGCTTCTGTGTGCTAGTGTCAATAATTAATGTA 311
    129 GAGCACTGGGCTATTATTAATGATGATTAAGTTGTGTGCTTGGAAATGACTTGT-- 186
QY 312 TTACAATGAGACTCTAGATGTGTGATCAAAAGAGATCTGTAACTGCACTGCA 371
    187 ----ACAAAGAGACCTTAATATGTGTGCTTCCGGGA---CTATTAGGGTCACTCCACAA 239
QY 372 CTTTGGCCCTCCCAATTTGGCCCTTCTTAACAACAATGAGGCTGGTCAACCACT 431
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Db 240 CTTTGGCCCTCCCAATTTGGCTCTCTTAACAACAATGAGGCTGGTCAACCACT 299
QY 432 CAAGCATTTTGAATATGAGCCCAACCGCTTGGGAAAAGATTGTATTTACAGAGAG 491
    300 CCAACACTTGACATGAGCTGAGCTGCTCTTCAATGCTCAATACCAAGCTGTAT 359
QY 492 CGTCCCGTGTCTATTTCAAAGGCTCCATGCAAAAAGCATGAGGAGTTAGTTCA 551
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Db 360 CGTCCCGTGTCTATTTCGATGAGGATCAATGATGAAGAAAGGTGAGTGAATTA 419
QY 552 GAAATGAGGAGCTACTTGTAGCTAGTATGATCAGCAATGTGGGGGTCTGATCAT 611
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QY 612 CCAATCAGTGTCAATTAAGGCTCAAAAAGCTGATGAGCAATGTCAAGAAATGG 671
    480 CCACTGTGTGCAATTAAGGAGGCTCGAACTGATGCAATCAATGTCTAAGAAATGG 539
QY 672 TTCTAATGAGCAATCCAAATCGTATTTGAATGTGCAATCTTGTCTTCAAGG 731
    540 CCAAACTGCAAGAGCAACAATCTATCTCAATGCGCAAGGCTTCTTCAAGTCA 599
QY 732 CACTGATGAGAGACCAAGATTTTCCAAATATTTTCCAGTATTTGCAATTTG 791
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QY 792 AACTTCTCTAGGCC 806
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Db 660 AACCTATGAAGGCC 674
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RESULT 3
US-09-362-642-1
; Sequence 1, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennet, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362.642
; EARLIER FILING DATE: 1999-07-27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum cv. 75
; FEATURE:

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Title: US-10-660-499A-1
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Scoring table: IDENTITY_NUC
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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	278.6	25.6	681	US-08-440-517A-1	Sequence 1, Appl1
2	278.6	25.6	681	US-09-092-160-1	Sequence 1, Appl1
3	216.6	19.9	702	US-09-362-642-1	Sequence 1, Appl1
4	215	19.7	702	US-08-845-539-1	Sequence 1, Appl1
5	188	17.3	537	US-08-845-539-5	Sequence 5, Appl1
6	188	17.3	537	US-09-362-642-5	Sequence 5, Appl1
7	187.4	17.2	727	US-07-885-970A-6	Sequence 6, Appl1
8	187.4	17.2	727	US-08-298-687A-6	Sequence 6, Appl1
9	187.4	17.2	727	US-08-530-797-5	Sequence 6, Appl1
10	187.4	17.2	727	US-08-298-829-6	Sequence 6, Appl1
11	187.4	17.2	727	US-08-787-335-5	Sequence 3, Appl1
12	181.4	16.7	501	US-08-845-539-3	Sequence 3, Appl1
13	181.4	16.7	501	US-09-362-642-3	Sequence 3, Appl1
14	145.2	13.3	2415	US-07-885-970A-26	Sequence 26, Appl1
15	145.2	13.3	2415	US-08-298-687A-26	Sequence 26, Appl1
16	145.2	13.3	2415	US-08-298-829-26	Sequence 26, Appl1
17	52	4.8	279	US-09-313-294A-1276	Sequence 1276, Ap
18	45.2	4.2	2128	US-08-415-593-39	Sequence 39, Appl1
19	44.6	4.1	640681	US-09-790-988-1	Sequence 1, Appl1
20	44.4	4.1	629	US-09-385-982-389	Sequence 389, App
21	44.2	4.1	1991	US-08-415-593-40	Sequence 40, Appl
22	44	4.0	1057	US-09-205-258-204	Sequence 204, App
23	44	4.0	1057	US-10-004-860-204	Sequence 204, App
24	44	4.0	194537	US-09-949-016-12928	Sequence 12928, A

C	25	44	4.0	201529	3	US-09-949-016-12740	Sequence 12740, A
C	26	43.2	4.0	3473	3	US-09-949-016-1148	Sequence 1148, Ap
C	27	43.2	4.0	53352	3	US-09-801-861-3	Sequence 3, Appl1
C	28	43.2	4.0	53332	3	US-10-224-562-3	Sequence 3, Appl1
C	29	43.2	4.0	53332	3	US-10-786-065-3	Sequence 3, Appl1
C	30	43	3.9	5852	2	US-07-867-106-2	Sequence 2, Appl1
C	31	42.8	3.9	32392	3	US-09-662-254B-27	Sequence 27, Appl1
C	32	42.8	3.9	50000	3	US-09-662-254B-23	Sequence 23, Appl1
C	33	42.6	3.9	1345	2	US-08-702-153-3	Sequence 1, Appl1
C	34	42.6	3.9	3704	2	US-08-702-153-1	Sequence 1, Appl1
C	35	42.6	3.9	60589	3	US-09-949-016-17070	Sequence 17070, A
C	36	42.4	3.9	789	9	5219739-8	Patent No. 5219739
C	37	42.2	3.9	1830	3	US-09-662-254B-67	Sequence 67, Appl1
C	38	42.2	3.9	32392	3	US-09-662-254B-27	Sequence 27, Appl1
C	39	42	3.9	3501	2	US-07-977-451-3	Sequence 3, Appl1
C	40	42	3.9	3501	2	US-08-252-517-3	Sequence 3, Appl1
C	41	42	3.9	3501	2	US-07-906-397A-3	Sequence 3, Appl1
C	42	42	3.9	3501	2	US-08-601-891-3	Sequence 3, Appl1
C	43	42	3.9	3501	2	US-09-021-324-3	Sequence 3, Appl1
C	44	42	3.9	3501	3	US-09-872-136B-3	Sequence 3, Appl1
C	45	42	3.9	3501	3	US-09-919-408A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1									
US-08-440-517A-1									
; Sequence 1, Application US/08440517A									
; Patent No. 5959082									
; GENERAL INFORMATION:									
; APPLICANT: COSGROVE, DANIEL J.;									
; APPLICANT: GULLITMAN, MARK;									
; APPLICANT: SHCHERBAN, TATYANA;									
; APPLICANT: SHI, JUN									
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS									
; NUMBER OF SEQUENCES: 6									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE									
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY									
; STREET: 113 TECHNOLOGY CENTER									
; CITY: UNIVERSITY PARK									
; STATE: PENNSYLVANIA									
; COUNTRY: UNITED STATES OF AMERICA									
; ZIP: 16802-7000									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: FLOPPY DISK									
; COMPUTER: NEC 286									
; OPERATING SYSTEM: DOS									
; SOFTWARE: WORDPERFECT 5.1									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/440,517A									
; FILING DATE:									
; CLASSIFICATION: 530									
; INFORMATION FOR SEQ ID NO: 1:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 681									
; TYPE: NUCLEIC ACID									
; STRANDEDNESS: SINGLE									
; TOPOLOGY: UNKNOWN									
; US-08-440-517A-1									
Query Match 25.6%; Score 278.6; DB 2; Length 681;									
Best local similarity 65.5%; Pred. No. 7.1e-66;									
Matches 442; Conservative 0; Mismatches 224; Indels 9; Gaps 2;									
QY	132	TGATGACCAACGCCCCATGCACTTTTATGCGGAGTGTGCTTCAGAACTATGG	191						
DB	9	TGCTGACAGAGCGGCACGCCACTTTATGTGTGTGACGACATCTGGCACATGGG	68						
QY	192	GGAGCTGTGGGTATGGGAATCTGTATGCAATCTGGTATGCAATGACATCTGAGTTT	251						
DB	69	TGAGCTGTGGGTATGGGAATTTATACGCCAAGGATATGGACAAACAGGTGGCGCT	128						


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; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49063
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Bovine 19866881334022
US-10-750-185-49063

Query Match
Best Local Similarity 52.8%; Pred. No. 2.4;
Matches 94; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 892 TTCTTCTGTTTTCATTTCCATCACTCCAGCCCTTATGACGATTAATTCCTTA 951
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DB 1037 TTTTACATATTTCTGGAATTTCTGTGTAACCTGAGTTTAATGCAAAATCAATAAAATTAC 1096

QY 952 TCAATATACAAATACACATCATATCATATCAATAGCTGTATATGAATTAACATCTT 1011
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DB 1097 ACCATTCACCATTTCTCCATCATATTAATTCGAAATCAATTAACGATTAACATGTT 1156

QY 1012 TCAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1069
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DB 1157 AATACGAAAAAATCAATTAATTTTAAATGTTTCATATTTATTTATGAAATTTCA 1214

RESULT 11
US-10-750-623-49063
; Sequence 49063, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49063
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Bovine 19866881334022
US-10-750-623-49063

Query Match
Best Local Similarity 4.0%; Score 43.6; DB 6; Length 1947;
Matches 94; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY 952 TCAATATACAAATACACATCATATCATATCAATAGCTGTATATGAATTAACATCTT 1011
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QY 1012 TCAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1069
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DB 1157 AATACGAAAAAATCAATTAATTTTAAATGTTTCATATTTATTTATGAAATTTCA 1214

RESULT 12
US-10-240-708-10/C
; Sequence 10, Application US/10240708
; Publication No. US20050282157A1
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; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-10

Query Match
Best Local Similarity 4.0%; Score 43.6; DB 6; Length 6070;
Matches 76; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 960 ACAATCAATCAGCATCATATCATATGCTTGATATCAATTAACATCTTCAAGTTT 1019
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DB 1867 AATATTAATATATATATATATATTTTACACAAATTAATTAATTAATTAATTAATTAATTA 1808

QY 1020 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1079
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1807 ACACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1748

QY 1080 AAAAAAAAAA 1089
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DB 1747 AAAAAAAAAA 1738

RESULT 13
US-10-786-065-3/C
; Sequence 3, Application US/10786065
; Publication No. US20040146924A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV II
; CURRENT APPLICATION NUMBER: US/10/786,065
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-065-3

Query Match
Best Local Similarity 4.0%; Score 43.2; DB 6; Length 53332;
Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 930 TCTATCAGGCAATTAATTTCTTATCATATATATATATATATATATATATATATATATATAT 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 31624 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 31565
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Query Match 4.1%; Score 45; DB 6; Length 2204;
Best Local Similarity 51.8%; Pred. No. 1.2;
Matches 102; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 892 TTCTCTGGTTTGGATTATCCCATCAACGCCCTGTATCAAGCATAAATCTTTA 951
DB 1740 TTATTAAGTATTGACTATGTTTCTACTCAGATGTTTCTCCTGTAACTCATTA 1799

QY 952 TCATATATACATCATCACCATCATATCATCTAGACTGTATATCAATTAACATCTT 1011
DB 1800 CAAAAAGTTAATTTCTCTTTCATCTCTCCCAACCAAGCAATCAATCCCATATAT 1859

QY 1012 TCAGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1071
DB 1860 TCAGGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1919

QY 1072 AAAAAAAAAAAAAAAAAA 1088
DB 1920 AAAAAAAAAAAAAAAAAA 1936

RESULT 8
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Greteardottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091.018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1

Query Match 4.1%; Score 44.2; DB 7; Length 1691140;
Best Local Similarity 57.7%; Pred. No. 11;
Matches 79; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 953 CAATATATACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCTTT 1012
DB 1658872 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1658813

QY 1013 CAAGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1072
DB 1658812 CAAGTTTCTTCT 1658753

QY 1073 AAAAAAAAAAAAAAAAAA 1089

DB 1658752 ATATTAACAAATTA 1658736

RESULT 9
US-10-240-708-33/c
; Sequence 33, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 33
; LENGTH: 5455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-33

Query Match 4.0%; Score 44; DB 6; Length 5455;
Best Local Similarity 52.1%; Pred. No. 2.6;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 902 TTGTATTTCCCATCAACCTCCAGCCCTGTATCAAGCATTAATCTTATCATATATAC 961
DB 1099 TTACTTATTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1040

QY 962 AATCAATCACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCTTTCAAGTTAA 1021
DB 1039 AATTTCTAACAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 980

QY 1022 ATTAATTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1081
DB 979 CTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 920

QY 1082 AAAAAAAAA 1089
DB 919 AAAAAA 912

RESULT 10
US-10-750-185-49063
; Sequence 49063, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482


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FEATURE:
NAME/KEY: misc.feature
LOCATION: (183)..(183)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (186)..(186)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (189)..(189)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (192)..(192)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (195)..(195)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (198)..(198)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (210)..(210)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (213)..(213)
OTHER INFORMATION: n is a, c, g, or t.
NAME/KEY: misc.feature
LOCATION: (222)..(222)
OTHER INFORMATION: n is a, c, g, or t.

Query Match 34.5%; Score 376.2; DB 6; Length 519;
Best Local Similarity 60.1%; Pred. No. 4.8e-72;
Matches 312; Conservative 113; Mismatches 94; Indels 0; Gaps 0;

QY 172 GATGCTTCAGAGAACTATGAGGAGGAGCTTGTGGTATGGAATCTGATGCAATGAGTAT 231
DB 1 GATGCMNSNGMNCNATGGGNGGNGNTGTGNTATGNAAYTNTATGCAAGTAT 60
QY 232 GGAATGAACTGAGCTTTAAGCATGCTTATTTAATGATGAGCTTCTGTGTGAT 291
DB 61 GGNACMNGMNCNGCNGNTMWSNACNGCNYTNTTAAAGYAGNGCWSNTGTGNCAR 120
QY 292 TGCTACAAATTTATGATGATTAAGATCAAGCTCTGATGATGATGATCAAGATCT 351
DB 121 TGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 352 GTAACCTTAATGCAAACTTTTGCCTCCCAATTTGCTTCTTCTTAAACAATGGA 411
DB 181 GTTACGNTMNCNGMNCNAAATTTTGTCTCNCNAAATTTGCTTCTTCTTAAACAATG 240
QY 412 GGTGTGTGCAACCCACCACTCAAGCATTTTGTATGAGCCCAACCGCTTGGGAAAAT 471
DB 241 GAGTGTGTAAACCCNCTTAAACATTTTGAATGAGCCCAACCGCTTGGGAAAAT 300
QY 472 GGTATTTACAGAGAGAGATGCTCCCGTGTATTTCAAAAGGTTTCAATGAAAAGAT 531
DB 301 GGNATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
QY 532 GGAAGGTTAGTTCAGTGTGATGATGAGAGGAGTCTTGTGATGATGATGATGAT 591
DB 361 GAGAGGTTAGTTCAGTGTGATGATGAGAGGAGTCTTGTGATGATGATGATGAT 420
QY 592 GTGGGGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
DB 421 GTGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 480
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QY 652 GCATGTCAAGAAATGGGGTCTTATGGAATCAAT 690
DB 481 GCATGWSMNGMNCNATGGGNGGNGNTGTGNTATGNAAYTNTATGCAAGTAT 519

RESULT 4
US-10-670-009-1
Sequence 1, Application US/10670009
Publication No. US20050272041A1
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J.
APPLICANT: Gullinan, Mark
APPLICANT: Shcherban, Tatyana
APPLICANT: Jun, Shi
TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
FILE REFERENCE: P0466US08
CURRENT APPLICATION NUMBER: US/10/670,009
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 09/896,301
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 09/429,675
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 08/834,327
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 08/444,515
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: US 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: US 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 681
TYPE: DNA
ORGANISM: Cucumis sativus
US-10-670-009-1

Query Match 25.6%; Score 278.6; DB 6; Length 681;
Best Local Similarity 65.5%; Pred. No. 5.1e-51;
Matches 442; Conservative 0; Mismatches 224; Indels 9; Gaps 2;

QY 132 TGAATGACCAAGCCATGCACTTTTATGAGGGATGATGATGATGATGATGATGAT 191
DB 9 TGAATGACCAAGCCATGCACTTTTATGAGGGATGATGATGATGATGATGATGAT 68
QY 192 GAGAGCTTGTGGTATGGAATCTGATGCAATGAGTATGAACTGCAAGCTTT 251
DB 69 TGAAGCTTGTGGTATGGAATCTGATGCAATGAGTATGAACTGCAAGCTTT 128
QY 252 AAGCATGCTTATTAATGATGAGAGCTTCTGTGTCACTGCTCAAAATTAATATG 311
DB 129 GAGCATGCTTATTAATGATGAGAGCTTCTGTGTCACTGCTCAAAATTAATATG 186
QY 312 TTACAATCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
DB 187 ----ACAAAGACCTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 239
QY 372 CTTTGGCTTCCCAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 431
DB 240 CTTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 299
QY 432 CAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
DB 300 CCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
QY 492 CGTCCCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 551
DB 360 CGTCCCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 419
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; SEQ ID NO 5
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Probe
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
; LOCATION: (39)..(39)
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; NAME/KEY: misc_feature
; LOCATION: (45)..(45)
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; NAME/KEY: misc_feature
; LOCATION: (51)..(51)
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; NAME/KEY: misc_feature
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; LOCATION: (87)..(87)
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
; LOCATION: (105)..(105)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108)..(108)
; OTHER INFORMATION: n is a, c, g, or t.
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; LOCATION: (111)..(111)
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; NAME/KEY: misc_feature
; LOCATION: (117)..(117)
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; NAME/KEY: misc_feature
; LOCATION: (150)..(150)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (159)..(159)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (174)..(174)
; OTHER INFORMATION: n is a, c, g, or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (177)..(177)
; OTHER INFORMATION: n is a, c, g, or t.
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; NAME/KEY: misc_feature
; LOCATION: (180)..(180)
; OTHER INFORMATION: n is a, c, g, or t.
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OY	181	GGAACTATGGGGGGAGCTGTGGGGTAATGGGAATCTGATGCAACTGGGTAATGAACCTAGA	240
Db	181	GGAACTATGGGGGGAGCTGTGGGGTAATGGGAATCTGATGCAACTGGGTAATGAACCTAGA	240
OY	241	ACTGCAGCTTTAAGCACTGCTTATTTATGATGAGAGCTTCTGTGTCAGTGTCTACAA	300
Db	241	ACTGCAGCTTTAAGCACTGCTTATTTATGATGAGAGCTTCTGTGTCAGTGTCTACAA	300
OY	301	ATTATATGTGATTCAAATCAGACTCTAGATGTGTGATCAAGAGAGATCTGTAAACGTA	360
Db	301	ATTATATGTGATTCAAATCAGACTCTAGATGTGTGATCAAGAGAGATCTGTAAACGTA	360
OY	361	ACTGCGCAAACTTTTGCCCTCCCAATTTGGCCCTTCTCTAACAAATGAGAGCTGTGTC	420
Db	361	ACTGCGCAAACTTTTGCCCTCCCAATTTGGCCCTTCTCTAACAAATGAGAGCTGTGTC	420
OY	421	AACCCACCACTCAAGCACTTTTGATATGTGSCCAACCCCGTTGGGAAAAAGATTGTATTAC	480
Db	421	AACCCACCACTCAAGCACTTTTGATATGTGSCCAACCCCGTTGGGAAAAAGATTGTATTAC	480
OY	481	AGAGAGGAGATCGTCCCGTGTCTATTTCAAAAGGTTCCATSCAAAAAGCATGAGAGGTT	540
Db	481	AGAGAGGAGATCGTCCCGTGTCTATTTCAAAAGGTTCCATSCAAAAAGCATGAGAGGTT	540
OY	541	AGGTTCAGTGTGAATGGAGGGACTACTTTGAGCTAGTATGATCAGCAATGTGGGGGT	600
Db	541	AGGTTCAGTGTGAATGGAGGGACTACTTTGAGCTAGTATGATCAGCAATGTGGGGGT	600
OY	601	GCTGGATCATCCCAATCAGTGTCTATTTAAAGGCTCAAAAACCTGATGTGACATGTCA	660
Db	601	GCTGGATCATCCCAATCAGTGTCTATTTAAAGGCTCAAAAACCTGATGTGACATGTCA	660
OY	661	AGAAATTTGGGGTCTTAATTTGGCAATCCAAATGCAATTTTGAATGTGCACTTTTGCTTC	720
Db	661	AGAAATTTGGGGTCTTAATTTGGCAATCCAAATGCAATTTTGAATGTGCACTTTTGCTTC	720
OY	721	AGGTCACCACTGATGAGAGACCAAGATTTTCCAAAGATTTGTTCCAGTAAAGTTGG	780
Db	721	AGGTCACCACTGATGAGAGACCAAGATTTTCCAAAGATTTGTTCCAGTAAAGTTGG	780
OY	781	ACATTCGGCCAAACCTTTCTTAAGCCCAATCAGTCTTAAGCTGATTAAGATTAACAAAC	840
Db	781	ACATTCGGCCAAACCTTTCTTAAGCCCAATCAGTCTTAAGCTGATTAAGATTAACAAAC	840
OY	841	CAACGGCTGAGCGCGTCTTTTATTTATTTAATTAAGAGCTGCCGCCACCCCTTCTTGG	900
Db	841	CAACGGCTGAGCGCGTCTTTTATTTATTTAATTAAGAGCTGCCGCCACCCCTTCTTGG	900
OY	901	TTTTGATTATTTCCATCAACTCCAAAGCCCTCTATCAGGCAATTAATTTATCAATATA	960
Db	901	TTTTGATTATTTCCATCAACTCCAAAGCCCTCTATCAGGCAATTAATTTATCAATATA	960
OY	961	CAATCAATCAGATATATCATCATTAAGCTGTATATCAATTAACATCTTTCAAGTTTA	1020
Db	961	CAATCAATCAGATATATCATCATTAAGCTGTATATCAATTAACATCTTTCAAGTTTA	1020
OY	1021	AATTAATTTAATCTAATAATGTGTAAATATCATATATGTTGAAGTTCAAAAAA	1080
Db	1021	AATTAATTTAATCTAATAATGTGTAAATATCATATATGTTGAAGTTCAAAAAA	1080
OY	1081	AAAAAAAAAAAA 1089	
Db	1081	AAAAAAAAAAAA 1089	
RESULT 2			
US-10-660-499A-7			
; Sequence 7, Application US/10660499A			
; Publication No. US20050246795A1			
; GENERAL INFORMATION:			
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION			
; APPLICANT: LEE, JONG SEOB			
; APPLICANT: LEE, DONG-KEUN			

```

1  APPLICANT: AHN, JI HOON
2  APPLICANT: SONG, SANG-KEE
3  APPLICANT: CHOI, YANG DO
4  TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
5  TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
6  FILE REFERENCE: 20020-02USA
7  CURRENT APPLICATION NUMBER: US/10/660,499A
8  CURRENT FILING DATE: 2003-09-12
9  PRIOR APPLICATION NUMBER: KR 2003-19069
10 PRIOR FILING DATE: 2003-03-27
11 NUMBER OF SEQ ID NOS: 9
12 SOFTWARE: Patentin version 3.3
13 SEQ ID NO 7
14 LENGTH: 389
15 TYPE: RNA
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: RNA probe (sense)
19 US-10-660-499A-7

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Query Match	35.7%	Score 389;	DB 6;	Length 389;
Best Local Similarity	69.4%;	Pred. No. 7.8e-75;		
Matches 270;	Conservative 119;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      603 TGGATCCATTCGAATCAGTGTTCATTAAAGGCTCAAAACTGATGATGGCAATGTCAAG 662
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      1   UGGAUCCAUCACUGAUGUUCAAUAAGAUGCACAAAAACUGAGUAGAUUGGCAUUGUCAAG 60
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Qy 663 AAATTGGGGTCTTAATTGGCAATCCATGCGTATTGATGGTCATCTTTCCTTCAG 722

Db 61 AAATUGGGGUCUAUUGGCAUCCAUUGCGUAUUGAUUGUCUAUCUUGUCCTUCAG 120

oy 723 GGTCAACCACTGATGAGAGACCAGAATTTCAGATAATTGGTCCAGTAAGTTGC 782

n 121 GGTTAACCAACTGATGAGAGACCAGAATTTCAGATAATTGGTCCAGTAAGTTGC 180

783 ATTCGGCACAATTCTCTAGCCCACTTCACTTCTAAGCTGATTACAGATAAACCAACA 8442

[illegible]

DB 241 ACCGCGAGCGCGCCUUUUUUUAUUAUGAGGACGCGCCCCCACCACCCUUUCUUGGU 300

DY 903 TTGATTATTCGCATCACTCCAAGCCCTGTACAAGCATATAATTCTATCATATAATACA 962

Db 301 TTGAAUUAUUTCCCAUCAUCUCCAGCCCTCUCAUACAAGSCAUAAUUCUUAUCAUAUAACA 366

Qy 963 ATCAATCACCATCATATCATCAAGAATT 991

Db 361 ATCAUCCACCAUUAUCAUCAUAAAGCUU 389

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RESULT 3
US-10-660-499A-5
; Sequence 5, Application US/10660499A
; Publication No. US20050246795A1

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; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG-KEUN

```

; APPLICANT: AHN, JI HOON
 ; APPLICANT: SONG, SANG-KEE
 ; APPLICANT: CHOI, YANG DO
 ; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND

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1 TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
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3 FILE REFERENCE: 2002-02USA
4
5 CURRENT APPLICATION NUMBER: US/10/660,499A
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7 CREATING DATE: 2002-06-12
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 ; CURRENT FILING DATE: 2003-03-12
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 ; PRIOR APPLICATION NUMBER: KR 2003-19069
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 ; PRIOR FILING DATE: 2003-03-27
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 ; NUMBER OF SEQ ID NOS: 9
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XX (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAOV/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
XX WPI; 2004-180133/17.
DR
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XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
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XX
XX Claim 1; SEQ ID NO 65439; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactamman,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX
XX Sequence 284 AA;
SQ
Query Match 74.3%; Score 1042; DB 8; Length 284;
Best Local Similarity 75.0%; Pred. No. 3e-96;
Matches 186; Conservative 24; Mismatches 38; Indels 0; Gaps 0;
QY 8 LGSIGLCCFTITTYAFSPSGMTNHAATFYGSDASGTMGACGYGNLYATGYGTRTAA 67
DB 36 LALLLAACILMKRACFSASGLNKAFATFYGSDASGTMGACGYGNLYSTGYGTRTAA 95
QY 68 STALFNDGASCGCCYKIIICDYKSDSRMCIKRSVYTTATNFCPPNFPALPNNNGKCNPP 127
DB 96 STALFNDGASCGCCYKIIICDYKSDSRMCIKRSVYTTATNFCPPNFPALPNNNGKCNPP 155
QY 128 KHEMDMOPAMEKIGIYRGIVPVLFORVPCKKHGVRFSVNGRDYFELVLIISNVGAGSI 187
DB 156 QHEMDMOPAMEKIGIYRGIVPVLFORVPCKKHGVRFSVNGRDYFELVLIISNVGAGSI 215
QY 188 QSVFIKSGKTGMAMSRNMGSNMOSNAYLNGOSLSFRVTTTDETRVFODIVPVSMTFGQT 247
DB 216 QSASIKSGRTGMAMSRNMGSNMOSNAYLNGOSLSFRVTTTDETRVFODIVPVSMTFGQT 275
QY 248 TRSSPVQF 255
DB 276 TRATSOQF 283
RESULT 15
ADJ92725
XX ADJ92725 standard; protein; 261 AA.
AC ADJ92725;
XX
XX 06-MAY-2004 (first entry)
XX
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DE Rice alpha-expansin protein.
XX Beta-expansin; cell wall expansion; cell wall loosening; paper industry;
XX paper recycling; rice; alpha-expansin.
XX
XX Oryza sativa.
XX
XX US6682738-B1.
XX
XX 27-JAN-2004.
XX
XX 01-MAY-1998; 98US-00071252.
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XX 02-MAY-1997; 97US-0045445P.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX Cosgrove DJ;
XX
XX WPI; 2004-118570/12.
XX
XX Composition comprising beta-expansin or its fragment induces expansion or
PT stress relaxation on grass cell walls more effectively than on
PT dicotyledon cell walls.
XX
XX Example 4; SEQ ID NO 36; 37pp; English.
XX
XX The invention relates to proteins belonging to a novel class of proteins
CC designated as beta-expansins. Beta-expansins have the property of
CC altering physical properties of a plant cell wall, such as loosening or
CC expanding plant cell walls. The invention is useful in paper industry for
CC paper recycling. The present sequence is rice alpha-expansin protein.
XX
XX
XX Sequence 261 AA;
SQ
Query Match 74.1%; Score 1039; DB 8; Length 261;
Best Local Similarity 73.2%; Pred. No. 5.3e-96;
Matches 180; Conservative 30; Mismatches 36; Indels 0; Gaps 0;
QY 10 SLIGLCCFTITTYAFSPSGMTNHAATFYGSDASGTMGACGYGNLYATGYGTRTAA 69
DB 15 ALLATCLLNNEAASFASGMNKAFATFYGSDASGTMGACGYGNLYSTGYGTRTAA 74
QY 70 ALFNDGASCGCCYKIIICDYKSDSRMCIKRSVYTTATNFCPPNFPALPNNNGKCNPP 129
DB 75 VLFNDGASCGCCYKIIICDYKSDSRMCIKRSVYTTATNFCPPNFPALPNNNGKCNPP 134
QY 130 FMDAOPAMEKIGIYRGIVPVLFORVPCKKHGVRFSVNGRDYFELVLIISNVGAGSI 189
DB 135 FMDAOPAMEKIGIYRGIVPVLFORVPCKKHGVRFSVNGRDYFELVLIISNVGAGSI 194
QY 190 VFIKSGKTGMAMSRNMGSNMOSNAYLNGOSLSFRVTTTDETRVFODIVPVSMTFGQT 249
DB 195 VSIKSGRTGMAMSRNMGSNMOSNAYLNGOSLSFRVTTTDETRVFODIVPVSMTFGQT 254
QY 250 SSPVQF 255
DB 255 STSOQF 260
Search completed: January 10, 2006, 12:35:01
Job time : 136 secs
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RESULT 11

ADY03869
ID ADY03869 standard; protein; 257 AA.

XX
XX ADY03869;

DT 21-APR-2005 (first entry)

XX Tobacco expansin, NtEXP3.

XX Expansin; plant; root; development; homology.

XX Nicotiana tabacum.

XX KR2004084166-A.

XX 06-OCT-2004.

XX 27-MAR-2003; 2003KR-00019069.

XX 27-MAR-2003; 2003KR-00019069.

XX (UYSE-) UNTV SEOUL NAT IND FOUND.

XX Ahn JH, Choi YD, Lee DG, Lee JS, Song SG;

XX WPI; 2005-108897/12.

PT Gene controlling root development of plant and method for manipulating
PT root development of plant using the same to improve phenotype of plant
PT related to root development and facilitate its growth.

PS Example 2; Fig 1; 27pp; Korean.

XX The present invention relates to Soybean gene GmEXPI coding sequence
CC (ADY03860), which encodes the protein expansin (ADY03861), which in turn
CC controls plant root development. The invention also relates to a method
CC for manipulating plant root development using GmEXPI expansin, to improve
CC the phenotype of a plant related to root development, and facilitating
CC the growth of it. Also disclosed are: recombinant vector pGA643/GmEXPI,
CC which contains gene GmEXPI; and a transformed bacterium produced by
CC transforming a bacterium with the recombinant vector pGA643/GmEXPI. The
CC method for facilitating the root development of a plant comprises
CC inserting the gene GmEXPI into the expression vector, and introducing the
CC expression vector into the plant. Proteins ADY03869-ADY03872 were used in
CC a sequence homology alignment along with protein ADY03861.

XX Sequence 257 AA;

Query Match 77.5%; Score 1087; DB 9; Length 257;

Best Local Similarity 75.3%; Pred. No. 7.5e-101; Indels 0; Gaps 0;

Matches 189; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 5 MLVLSLIGLCPTITTYAFSPSGWTNNAATFYGSDASGTMGACGYGLVATGYGRT 64

DB 6 IIALGRIIGPFSIFFNANAFTASGMRAHATFTGADASTMGACGYGLVSTGYGTS 65

QY 65 AALSTLFLFNDASCGGCTYKICDYKDSRWICGRSVTTTAINFCPPNFPALPNNNGKCN 124

DB 66 AALSTLFLFNDASCGGCTYKICDYKDSRWICGRSVTTTAINFCPPNFPALPNNNGKCN 125

QY 125 PLPKHDMQAPAEKIGIYRGIVPVLFOKVPCKKGGVAFSNGRDYFLVVISVVGGA 184

DB 126 PPKHDMQAPAEKIGIYRGIVPVLFOKVPCKKGGVAFSNGRDYFLVVISVVGGA 185

QY 185 GSISQVFIKSGKTMAMSNMGSNNQSNAYLNGOSLSFVTTTDDETRFQDIVESWT 244

DB 186 GSISQVFIKSGKTMAMSNMGSNNQSNAYLNGOSLSFVTTTDDETRFQDIVESWT 245

QY 245 FGQTSSPVQF 255

DB 246 FGQTSSPVQF 256

RESULT 12

ADY08132
ID ADY08132 standard; protein; 273 AA.

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XX ADY08132;

DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 63947.

XX plant protectant; plant growth regulant; gene therapy; plant;

XX recombinant DNA construct; physical array; plant breeding marker;

XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;

XX growth rate; cell cycle pathway; disease resistance;

XX galactomanan production; lignin production; plant growth regulator;

XX yield; plant growth; plant development; seed oil; protein yield;

XX protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TAB/) TABASKA J E.

XX (CAO/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX Claim 1; SEQ ID NO 63947; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomanan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.

XX Sequence 273 AA;

Query Match 74.3%; Score 1043; DB 8; Length 273;

Best Local Similarity 75.0%; Pred. No. 2.2e-96;

PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157113P.
 PR 05-OCT-1999; 99US-0157757P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 77.8%; Score 1092; DB 3; Length 252;
 Best Local Similarity 78.6%; Pred. No. 2.3e-101;

Matches 195; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 8 LGSLLIGLCCFTITTYAFSPSGWTNATFYGSDASGTMGACGYGNLYATGYGTRTAAI 67
 DB 5 LAGLAVLALFLAVDAFKPSGLTNGHATFYGSDASGTMGACGYGDLVSAGYGTAAI 64
 QY 68 STALFNDGASCGCCYKIIICDYKDSRWCTKGSVYTTATNFCPPNLPALPNNNGWKNPPL 127
 DB 65 STALFNDGASCGCCYKIIICDYKDSRWCTKGSVYTTATNFCPPNLPALPNNNGWKNPPL 124
 QY 128 KHFDMAPAMEKIGIRGGIVPVLFORVPCKKHGVRFSVNGRDYFELVLISNVGAGSI 187
 DB 125 KHFDMAPAMEKIGIRGGIVPVLFORVPCKKHGVRFSVNGRDYFELVLISNVGAGSI 184
 QY 188 QSVFIKSGTKTGMAMSRNMGSNWQSNAYLNGSLSPFRVTTTDDETRFDIVPVSMTFQ 247
 DB 185 KSVSIKSGTKTGMAMSRNMGSNWQSNAYLNGSLSPFRVTTTDDETRFDIVPVSMTFQ 244
 QY 248 TRSSPYQF 255
 DB 245 IYSSNVQF 252

RESULT 10
 ADN74397 standard; protein; 252 AA.

XX ADN74397;
 XX DT 15-JUL-2004 (first entry)
 XX Thale cress protein repressed in E2Fa/Dpa expressing plants Segid 2292.
 XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 KW animal feed product; thale cress; cell wall biosynthesis;

KW nitrogen metabolism; carbon metabolism.
 XX Arabidopsis thaliana.
 OS WO2004035798-A2.
 XX 29-APR-2004.
 PD 20-OCT-2003; 2003WO-BP011658.
 PF 18-OCT-2002; 2002EP-00079408.
 PR (CROP-) CROPPDESIGN NV.
 XX Inze D, De Veylder L, Vlieghe K;
 XX WPI, 2004-348466/32.
 DR N-PSDB; ADN74396.
 XX Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.

Claim 1, SEQ ID NO 2292; 134pp; English.

XX This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene repressed 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 CC invention.

XX Sequence 252 AA;

Query Match 77.8%; Score 1091; DB 8; Length 252;
 Best Local Similarity 78.6%; Pred. No. 2.9e-101;

Matches 195; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 8 LGSLLIGLCCFTITTYAFSPSGWTNATFYGSDASGTMGACGYGNLYATGYGTRTAAI 67
 DB 5 LAGLAVLALFLAVDAFKPSGLTNGHATFYGSDASGTMGACGYGDLVSAGYGTAAI 64
 QY 68 STALFNDGASCGCCYKIIICDYKDSRWCTKGSVYTTATNFCPPNLPALPNNNGWKNPPL 127
 DB 65 STALFNDGASCGCCYKIIICDYKDSRWCTKGSVYTTATNFCPPNLPALPNNNGWKNPPL 124
 QY 128 KHFDMAPAMEKIGIRGGIVPVLFORVPCKKHGVRFSVNGRDYFELVLISNVGAGSI 187
 DB 125 KHFDMAPAMEKIGIRGGIVPVLFORVPCKKHGVRFSVNGRDYFELVLISNVGAGSI 184
 QY 188 QSVFIKSGTKTGMAMSRNMGSNWQSNAYLNGSLSPFRVTTTDDETRFDIVPVSMTFQ 247
 DB 185 KSVSIKSGTKTGMAMSRNMGSNWQSNAYLNGSLSPFRVTTTDDETRFDIVPVSMTFQ 244
 QY 248 TRSSPYQF 255
 DB 245 IYSSNVQF 252

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 23-APR-1999; 99US-0130510P.
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SQ Sequence 255 AA;

Query Match 100.0%; Score 1403; DB 9; Length 255;
 Best Local Similarity 100.0%; Pred. No. 9, 7e-133;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKIMLVLSLIGLCCFTTTTAAFSPSGWTNAHATFYGSDASGTWGAAGYGNLYATGY 60
 DB 1 MGKIMLVLSLIGLCCFTTTTAAFSPSGWTNAHATFYGSDASGTWGAAGYGNLYATGY 60
 QY 61 GTRTAAALSTALFNDGASCCGCKYKIIDYKSDSRWCIGKRSVYTATNFCPPNLPNNNG 120
 DB 61 GTRTAAALSTALFNDGASCCGCKYKIIDYKSDSRWCIGKRSVYTATNFCPPNLPNNNG 120
 QY 121 GWCNPLPKFDMAPAMKIGIRGGIVPLFORVPCCKHGGVRFVNGRDYBELVLISN 180
 DB 121 GWCNPLPKFDMAPAMKIGIRGGIVPLFORVPCCKHGGVRFVNGRDYBELVLISN 180
 QY 181 VGGAGSIQSVFIKSGTGMAMSRNMGSNWQSNAYLNGSLSPRYTTDGETRVPDIIYV 240
 DB 181 VGGAGSIQSVFIKSGTGMAMSRNMGSNWQSNAYLNGSLSPRYTTDGETRVPDIIYV 240
 QY 241 VSWTFGQTFSSPYQF 255
 DB 241 VSWTFGQTFSSPYQF 255

RESULT 2
 ADX88821
 ID ADX88821 standard; protein; 263 AA.

XX ADX88821;
 DT 21-APR-2005 (first entry)
 XX Plant full length insect polypeptide seqid 51485.
 XX
 DE plant protectant; plant growth regulator; gene therapy; plant;
 XX recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomanan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS unidentified.
 OS
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX

PA (LITU/) LITU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S B.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR MPI; 2004-180133/17.
 XX

PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX

PS Claim 1; SEQ ID NO 51485; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomanan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX

SQ Sequence 263 AA;

Query Match 99.7%; Score 1399; DB 8; Length 263;
 Best Local Similarity 99.6%; Pred. No. 2, 6e-132;
 Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKIMLVLSLIGLCCFTTTTAAFSPSGWTNAHATFYGSDASGTWGAAGYGNLYATGY 60
 DB 9 MGKIMLVLSLIGLCCFTTTTAAFSPSGWTNAHATFYGSDASGTWGAAGYGNLYATGY 68
 QY 61 GTRTAAALSTALFNDGASCCGCKYKIIDYKSDSRWCIGKRSVYTATNFCPPNLPNNNG 120
 DB 69 GTRTAAALSTALFNDGASCCGCKYKIIDYKSDSRWCIGKRSVYTATNFCPPNLPNNNG 128
 QY 121 GWCNPLPKFDMAPAMKIGIRGGIVPLFORVPCCKHGGVRFVNGRDYBELVLISN 180
 DB 129 GWCNPLPKFDMAPAMKIGIRGGIVPLFORVPCCKHGGVRFVNGRDYBELVLISN 188
 QY 181 VGGAGSIQSVFIKSGTGMAMSRNMGSNWQSNAYLNGSLSPRYTTDGETRVPDIIYV 240
 DB 189 VGGAGSIQSVFIKSGTGMAMSRNMGSNWQSNAYLNGSLSPRYTTDGETRVPDIIYV 248
 QY 241 VSWTFGQTFSSPYQF 255
 DB 249 ASWTFGQTFSSPYQF 263

RESULT 3
 AAE00413
 ID AAE00413 standard; protein; 257 AA.

XX AAE00413;
 DT 19-JUN-2001 (first entry)
 XX
 DE Tomato seed expansion, leExp8, for controlling seed germination.
 XX

XX Tomato; endo-beta-mannanase; Lycopersicon esculentum mannanase2; leMAN2;
 KW polygalacturonase; Pg; leExp1; cellulase; arabinosidase; leAR1;
 KW xyloglucan endotransglycosylase; XET; leXET4; expansin; leEXP8;
 KW leEXP10; hydrolase; endosperm cap; tissue weakening; radicle growth;
 KW seed germination.
 XX

XX Lycopersicon esculentum.

XX WO200123530-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-US026884.

XX 30-SEP-1999; 99US-00410191.

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OM protein - protein search, using sw model

Run on: January 10, 2006, 12:17:13 ; Search time 133 Seconds
(without alignments)
842.418 Million cell updates/sec

Title: US-10-660-499A-2

Perfect score: 1403

Sequence: 1 MGKIMVLQSLGLCCFTT.....QDIVPVSWTFGQTFSSPVQF 255

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403	100.0	255	9 ADY03861	Ady03861 Soybean e
2	1399	99.7	263	8 ADX88821	Adx88821 Plant ful
3	1110.5	79.2	257	4 AAB00413	Aae00413 Tomato se
4	1103.5	78.7	258	8 ADJ92712	Adj92712 Cucumis s
5	1103.5	78.7	258	8 ADQ92317	Adq92317 Cucumber
6	1103.5	78.7	258	9 ADY03870	Ady03870 Cucumber
7	1098.5	78.3	266	3 AAG26695	Aag26695 Arabidops
8	1097.5	77.8	234	8 ADG48110	Adg48110 Plant exp
9	1092	77.8	252	3 AAG26696	Aag26696 Arabidops
10	1091	77.8	252	8 ADN74397	Adn74397 Thale cre
11	1087	77.5	257	9 ADY03869	Ady03869 Tobacco e
12	1043	74.3	273	8 ADY08132	Ady08132 Plant ful
13	1043	74.3	273	8 ADX89881	Adx89881 Plant ful
14	1042	74.3	284	8 ADY09624	Ady09624 Plant ful
15	1039	74.1	261	8 ADJ92725	Adj92725 Rice alph
16	1039	74.1	261	8 ADQ92330	Adq92330 Rice alph
17	978	69.7	210	3 AAG26697	Aag26697 Arabidops
18	923	65.8	223	5 ABB98474	Abb98474 Plant exp
19	923	65.8	223	8 ADG48107	Adg48107 Trichoder
20	913	64.3	264	8 ADX80240	Adx80240 Plant ful
21	901.5	64.3	222	8 ADG48108	Adg48108 Plant exp
22	898	64.0	249	3 AAG51646	Aag51646 Arabidops
23	898	64.0	249	3 AAG51632	Aag51632 Arabidops
24	898	64.0	249	3 AAG06545	Aag06545 Arabidops

25	898	64.0	249	8 ADT56553	Adt56553 Plant pol
26	898	64.0	259	3 AAG06544	Aag06544 Arabidops
27	898	64.0	259	3 AAG51631	Aag51631 Arabidops
28	898	64.0	280	3 AAG51645	Aag51645 Arabidops
29	893	63.6	193	3 AAG20642	Aag20642 Arabidops
30	892.5	63.6	277	8 ADX74868	Adx74868 Plant ful
31	892	63.6	241	3 AAG51633	Aag51633 Arabidops
32	892	63.6	241	3 AAG51647	Aag51647 Arabidops
33	892	63.6	241	3 AAG06546	Aag06546 Arabidops
34	890.5	63.5	254	8 ADJ92726	Adj92726 Arabidops
35	890.5	63.5	254	8 ADQ92331	Adq92331 Arabidops
36	889	63.4	227	2 AAR94527	Aar94527 Cucumber
37	889	63.4	227	5 AAG80768	Aag80768 C. sativu
38	888.5	63.3	226	5 AAG80769	Aag80769 C. sativu
39	886.5	63.2	250	8 ADJ92711	Adj92711 Cucumis s
40	886.5	63.2	250	8 ADQ92316	Adq92316 Cucumber
41	885	63.1	249	8 ADX79301	Adx79301 Plant ful
42	884.5	63.0	228	2 AAR94528	Aar94528 Rice expa
43	882	62.9	251	3 AAG23852	Aag23852 Arabidops
44	882	62.9	253	3 AAG23851	Aag23851 Arabidops
45	882	62.9	282	3 AAG23850	Aag23850 Arabidops

ALIGNMENTS

RESULT 1
ID ADY03861 standard; protein; 255 AA.
XX ADY03861;

AC ADY03861;

DT 21-APR-2005 (first entry)

XX Soybean expansin, GmEXPI, SEQ ID 2.

DE GmEXPI; expansin; plant; root; development.

XX GmEXPI max.

OS glycine max.

PN KR2004084186-A.

XX 27-MAR-2003; 2003KR-00019069.

PF 27-MAR-2003; 2003KR-00019069.

XX 27-MAR-2003; 2003KR-00019069.

PR (UYSR-) UNIV SEOUL NAT IND FOUND.

XX Ahn JH, Choi YD, Lee DG, Lee JS, Song SG;

XX WPI; 2005-108897/12.

DR N-PSDB; ADY03860.

XX Gene controlling root development of plant and method for manipulating

PT root development of plant using the same to improve phenotype of plant

PT related to root development and facilitate its growth.

PS Claim 1; SEQ ID NO 2; 27pp; Korean.

XX The present invention relates to Soybean gene GmEXPI coding sequence

CC (ADY03860), which encodes the protein expansin (ADY03861), which in turn

CC controls plant root development. The invention also relates to a method

CC for manipulating plant root development using GmEXPI expansin, to improve

CC the phenotype of a plant related to root development, and facilitating

CC the growth of it. Also disclosed are: recombinant vector pGA643/GmEXPI,

CC which contains gene GmEXPI; and a transformed bacterium produced by

CC transforming a bacterium with the recombinant vector pGA643/GmEXPI. The

CC method for facilitating the root development of a plant comprises

CC inserting the gene GmEXPI into the expression vector, and introducing the

CC expression vector into the plant.

Qy 28 GWTNAHATFYGGSDASGTWGAAGYGNLYATGYTRTALSTALFNDGASCGQCYKIICD 87
 Db 35 GWQTAHATFYGGADATGTWGAAGYGNLYSGYGTSTALSTALFNNHLSGAGCYELRCN 94
 Qy 88 YKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGWGCNPPKHPDMAQAPAMEKIGIYRGCI 147
 Db 95 --NDPQWCI-SRTITVTATNFCPPNYALSSDNGWGCNPREHFDLAEPFLRIABYRAGI 151
 Qy 148 VPVLFQRPVCKKHGVRFSVNGRDYFELVLSNVGAGSISQVFIKGSKTGMAMSRNWG 207
 Db 152 VPVMPFRVRVSCVKKGIRYTMNGHSYFNMYLITKLGAGADITSVISIKGSRTGMLPMSRWNG 211
 Qy 208 SNMOSNAYLNGOSLSFPRVTTTDDETFRVPODIVPVSWTFGQTF 249
 Db 212 QNMOSNAYLNGOSLSFVKVTASDGRITTAIVNVPAQWQFQTF 253

Search completed: January 10, 2006, 12:38:42
 Job time : 39 secs

A:Introns: 46/1
A>Note: T15B16.16
C:Superfamily: Major pollen allergen/expansion

Query Match 62.3%; Score 874; DB 2; Length 255;

Best Local Similarity 61.7%; Pred. No. 1.9e-67;

Matches 158; Conservative 38; Mismatches 58; Indels 2; Gaps 2;

QY 1 MGKIMLVLSGLGCGFTITTYA PPSGWTNAHATPYGSDASGTMGACGYGNLYATGY 60

DB 1 MKXIFSLVAMIFSTMFPMKISSVS -AGMLQAHATFGSDASGTMGACGYGNLYATGY 59

QY 61 GRTTALSTRLEFNDGASCCGCTYKIDYKDSRWCKIKGRSVYTTATNFCPPNALPNNNG 120

DB 60 KNTTAAALSTALFNDGASCCGCTYKIDYKDSRWCKIKGRSVYTTATNFCPPNALPNNNG 119

QY 121 GNCNPLKPFDMQAPMEKIGIRGGIVPVLFORVPCCKHGGVRSVNGRDYELVLI 180

DB 120 GNCNPRPRHDMQAPPLTAKTKAGIVPILYKVGCRSGGMRFTINGRNYELVLI 179

QY 181 VGGAGSIQSVFIKSGKTG -WMAMSRNMGSNMGSNAYLNGSLSPRYTTDGETRVQDIY 239

DB 180 VAGGSIKSVYKIGSKSNKMETSRMVGANYQSNYTLNGSLSPRYTTDGETRVQDIY 239

QY 240 PVSMTGQTFSSPVQF 255

DB 240 PSNMRFGQSFKSNVP 255

RESULT 13

expansin EXP2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004

C:Accession: T50656

R.Shcherban, T.Y.; Shi, J.; Dzuracko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh,

Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi-

A:Reference number: Z14894; PMID:96016146; PMID:7568110

A:Accession: T50656

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <SHC>

A:Cross-references: UNIPROT:Q38866; UNIPARC:UPI0000012A38E; EMBL:U30481; PIDN:AA838073.1

A:Experimental source: variety Columbia

C:Genetics:

A:Gene: EXP2

A:Function: induces extension (creep) in plant cell walls

A:Superfamily: Major pollen allergen/expansion

C:Keywords: cell wall

Query Match 61.5%; Score 863.5; DB 2; Length 255;

Best Local Similarity 63.6%; Pred. No. 1.5e-66;

Matches 154; Conservative 32; Mismatches 49; Indels 7; Gaps 4;

QY 12 IGLCFTITTYAFSP---SGMTNAHATPYGSDASGTMGACGYGNLYATGYGRTTALS 68

DB 12 LSLCTINPCLYINSNDNGMERGHATFYGADASGTMGACGYGNLYATGYGRTTALS 71

QY 69 TALFNDGASCGQCYKIIDYKDSRWCKIKGRSVYTTATNFCPPNALPNNNGCNPPLK 128

DB 72 TALFNSGQKCGACFELTCE--DDPEWCIPG-SIIVSKTNFCPPNFALANDNGCNPPLK 128

QY 129 HPMAPAMEKIGIRGGIVPVLFORVPCCKHGGVRSVNGRDYELVLI 188

DB 129 HPLAPAPLQIAQYPAAGIVPAFRVPCCKHGGVRSVNGRDYELVLI 188

QY 189 SVFIKSGKTG-WMAMSRNMGSNMGSNAYLNGSLSPRYTTDGETRVQDIY 247

DB 189 AVSLKSKTDQMSRSMNGMNSYTLNGSLSPRYTTDGETRVQDIY 248

QY 248 TF 249

DB 249 TF 250

RESULT 14

F84831

probable expansin [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004

C:Accession: F84831

R.Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

ues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: F84831

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: UNIPROT:Q22874; UNIPARC:UPI000000141E; GB:AE002093; NID:92651297; P

A:Gene: At2g40610

C:Genetics:

A:Map position: 2

C:Superfamily: Major pollen allergen/expansion

Query Match 61.4%; Score 862; DB 2; Length 253;

Best Local Similarity 68.2%; Pred. No. 2e-66;

Matches 152; Conservative 27; Mismatches 40; Indels 4; Gaps 3;

QY 28 GWTNAHATPYGSDASGTMGACGYGNLYATGYGRTTALSTRLEFNDGASCCGCTYKID 87

DB 29 GQGGHATPYGSDASGTMGACGYGNLYATGYGRTTALSTRLEFNDGASCCGCTYKID 88

QY 88 YKSDSRKIKGRSVYTTATNFCPPNALPNNNGCNPPLKPFDMQAPMEKIGIRGGI 147

DB 89 --DDPRKCL-GSITTTATNFCPPNGLSNDNGMKNPPLQHFDAEPALQIAQYRAGI 145

QY 148 VPVLFGRVPCCKHGGVRSVNGRDYELVLI 206

DB 146 VPVSPFRVPCCKHGGVRSVNGRDYELVLI 205

QY 207 GSNMGSNAYLNGSLSPRYTTDGETRVQDIY 249

DB 206 GQNMGSNAYLNGSLSPRYTTDGETRVQDIY 248

RESULT 15

T09786

expansin - upland cotton

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004

C:Accession: T09786

R.Orford, S.J.; Timmis, J.N.

Biochim. Biophys. Acta 1398, 342-6, 1998

A:Title: Specific expression of an expansin gene during elongation of cotton fibres.

A:Reference number: Z14468; PMID:9655931; PMID:9655931

A:Accession: T09786

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-258 <ORF>

A:Cross-references: UNIPROT:Q49194; UNIPARC:UPI000009E557; EMBL:AF043284; NID:92811277;

A:Experimental source: cultivar Siokra 1-2

C:Genetics:

A:Gene: GhEX1

A:Function: involved in cell wall modification

A:Superfamily: Major pollen allergen/expansion

Query Match 61.1%; Score 857.5; DB 2; Length 258;

Best Local Similarity 66.7%; Pred. No. 5e-66;

Matches 148; Conservative 34; Mismatches 37; Indels 3; Gaps 2;

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C:Accession: T50654
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
A:Reference number: Z14894; MID:96016146; PMID:7568110
A:Accession: T50654
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-237 <SHC>
A:Cross-references: UNIPROT:Q9C554; UNIPARC:UPI00001553E4; EMBL:U30476; PIDN:AAB38070.1
C:Genetics:
A:Gene: EXP1
C:Function: induces extension (creep) in plant cell walls
C:Superfamily: Major pollen allergen/expansion
C:Keywords: cell wall

Query: Match 63.5%; Score 890.5; DB 2; Length 237;
Best Local Similarity 66.5%; Pred. No. 6,9e-69;
Matches 151; Conservative 35; Mismatches 38; Indels 3; Gaps 2;

QY 24 FSPSGWTNAHATFYGGSDASGTMGACGYGNLYATGYGRTAALSTALFNDDGASCGCYK 83
DB 9 YAGCGVNAHATFYGGSDASGTMGACGYGNLYSGYGTNTAALSTALFNDDGASCGACE 68
QY 84 IICDYKSDRMCIKGRSVTVTATNFCPPFPALPNNNGMCPPLKHFDPMAQPAWEKIGIY 143
DB 69 IRC--ONDGKWCILPG-SIVVTATNFCPPFPALPNNNGMCPPLKHFDPMAQPAWEKIGIY 125
QY 144 RGIIVVULFORVCKKHGVRFSVNGRDYDELVLISNNGAGSIOGVFKSGTGMAMS 203
DB 126 RAGIVVAARVRPCVRRGGIRFTINGHSYFNLVLINVGAGGVHAMKSGSKTGMQAMS 185
QY 204 RNMGMOSNAYNLGQSLSFRTVTTTDETRVFODIYVPSWTFQTPS 250
DB 186 RNMGMOSNAYNLGQSLSFRTVTTTDETRVFODIYVPSWTFQTPS 232

RESULT 10
T03298
expansin 2 - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C:Accession: T03298
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
A:Reference number: Z14894; MID:96016146; PMID:7568110
A:Accession: T03298
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-251 <SHC>
A:Cross-references: UNIPROT:Q40636; UNIPARC:UPI000009C8D9; EMBL:U30477; NID:G1041709; PI
C:Genetics:
A:Gene: EXP2
C:Function: induces extension (creep) in plant cell
C:Superfamily: Major pollen allergen/expansion

Query Match 62.7%; Score 879.5; DB 2; Length 251;
Best Local Similarity 64.4%; Pred. No. 6,4e-68;
Matches 154; Conservative 29; Mismatches 53; Indels 3; Gaps 2;
QY 11 LIGLCCFTITTYAFSPSGWTNAHATFYGGSDASGTMGACGYGNLYATGYGRTAALST 70
DB 11 LFAFPCFARARAAADVGSMGSAHATFYGGSDASGTMGACGYGNLYSTGYGTNTAALST 70
QY 71 LFNDDGASCGCYKIICDYKSDRMCIKGRSVTVTATNFCPPFPALPNNNGMCPPLKHF 130
DB 71 LFNDDGASCGCYKIICDYKSDRMCIKGRSVTVTATNFCPPFPALPNNNGMCPPLKHF 127

QY 131 DMAQPAWEKIGIYRGIVPVLFORVCKKHGVRFSVNGRDYDELVLISNNGAGSIOGV 190
DB 128 DMAEPAFQIGVYRAGIVPVSVRYRVPCKGKGIREFTINGHSYFNLVLINVGAGPDVDSV 187
QY 131 PIKSGKTGMAMSRWGSNNQSNALINQSLSFRTTDDGRTVODIYVPSWTFQTP 249
DB 188 SIKSGSTGMQPMRNMWGNQSNALINQSLSFQVAVSDGRTVTSNNVVPAGMDFXQTP 246

RESULT 11
C84444
Probable expansin (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: C84444
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L. eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MID:20083487; PMID:10617197
A:Accession: C84444
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: UNIPROT:Q80622; UNIPARC:UPI000012A2B5; GB:AE002093; NID:G3461833; PI
C:Genetics:
A:Gene: At2g03090
A:Map position: 2

Query: Match 62.5%; Score 876.5; DB 2; Length 248;
Best Local Similarity 62.7%; Pred. No. 1,1e-67;
Matches 153; Conservative 35; Mismatches 49; Indels 7; Gaps 3;

QY 11 LIGLCCFTITTYAFSPSGWTNAHATFYGGSDASGTMGACGYGNLYATGYGRTA 66
DB 3 LIGLALFCFPAWVCSVHYDAGVNAHATFYGGSDASGTMGACGYGNLYSGYGTNTA 62
QY 67 LSTALFNDDGASCGCYKIICDYKSDRMCIKGRSVTVTATNFCPPFPALPNNNGMCP 126
DB 63 LSTALFNDDGASCGACEIKC--QSDGAWCLPG-ALIVTATNFCPPFPALPNNNGMCP 119
QY 127 LKHFDPMAQPAWEKIGIYRGIVPVLFORVCKKHGVRFSVNGRDYDELVLISNNGAGS 186
DB 120 LKHFDPDSQVPRQIRAGYKGVVPVGYRYPVPCRRGIRFTINGHSYFNLVLINVGAGD 179
QY 187 IOSVPIKSGKTGMAMSRWGSNNQSNALINQSLSFRTTDDGRTVODIYVPSWTFQ 246
DB 180 VHSVAVKSGRTWQMSRWGNQSNALINQSLSFRTVADSGRTVTSNNVVPAGMDFXQTP 239
QY 247 QTPS 250
DB 240 QTPS 243

RESULT 12
T02010
expansin homolog T15B16.16 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 31-Dec-2004
C:Accession: T02010
R:Stoneking, T.; Smith, R.
Submitted to the EMBL Data Library, November 1998
A:Description: The sequence of A. thaliana T15B16.
A:Reference number: Z14488
A:Accession: T02010
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-255 <STO>
A:Cross-references: UNIPROT:Q9Z511; UNIPARC:UPI000012A2B7; EMBL:AF104919; NID:G3859590;
A:Experimental source: Cultivar Columbia
C:Genetics:
A:Map position: 4

	Matches	161; Conservative	28; Mismatches	37; Indels	3; Gaps	2;
Qy	21	TYAFSPGWNAAHATFYGSDASGTMGACGYNLYATGYGTRTALSTALFNDGASCGQ	80			
Db	2	TGAHGYGWMESAHAATFYGGSDASGTMGACGYGNLYSGOYGTNTTALSTALFNDGLSCGA	61			
Qy	81	CYKII CDKPSDRMOKIGRSYTVTA TNFCPPHFALPNNNGCHCNPLGHFPMADAPAMKTI	140			
Db	62	CYEMQCN--DDPQWCLPG-TVTVTA TNFCPPNNALPNNNGCHCNPLGHFPMADAPAFUKI	118			
Qy	141	GIYRGAI PVL FQRPCKKHGGVRFPSVNGRDVFLVLLISNVCAGASIQSIFIKSGTKTMM	200			
Db	119	AKYRGIPILITRYPCILARKGIRFTVNGHSIFNLVLTITNNGADVANAIVSKSGRSQWQ	178			
Qy	201	AMSRWGSNMQSNAYLNGQSLSFRTVTTDGETRFQDIVPVSWTGCQTF	249			
Db	179	PMSRWGQNMQSNSTLNGQSLSFQVTTSDGRVTVSNNNVAPSPMWCQGF	227			

RESULT 6
 T09818
 expansin (clone pPexp2) - 10b1011y pine (fragment)
 C.Species: Pinus taeda (10b1011y pine)
 C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
 C.Accession: T09818
 R.Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A.Description: Expansins are conserved in conifers and expressed in response to exogenous
 A.Reference number: Z16866
 A.Accession: T09818
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-232 <HUT>
 A.Cross-references: UNIPROT:P93492, UNIPARC:UPI00000A64BF, EMBL:U64890, NID:g1778098, P

Query Match	64.6%	Score 906.5	DB 2	Length 232
Best Local Similarity	70.3%	Pred. No. 2.9e-70		
Matches	161	Conservative	27	Mismatches 38; Indels 3; Gaps 2
QY	21	TYAFSPSMTNAHAATFYGGSDASGTMGACCGYGLYANGYGRALSTALFNDGASGQ	80	
Db	2	TGAHGYGWMESHAHATFYGGSDASGTMGACCGYGLYANGYGRNTALSTALFNDLSGCA	61	
QY	81	CYKIIDCYKSSRWICIKGRSVTYTATNTFCPPNFALPNNNGCKNCPPLKHPMAQPAWEKI	140	
Db	62	CYEMKCN--DDPQWCLPG--TYVTATNTFCPPNNALPNNNGCKNCPPLQHPMAEAPAFIKI	118	
QY	141	GIYRGCIIPVLFQRPCKKHGGVRFPSVANGRDYDFELVLLISNYGAGSIQSIFLKSKTGM	200	
Db	119	AKYRGCIPIILYTRPCLRKRGIRFTVANGHSIFNLVLLITNNGAGDVANVASIKSMSCNQ	178	
QY	201	AMSRNWSNMQSNAYLNGQSLSFRVYTTDGETRFPQDIVPVSWTGGTF	249	
Db	179	PMSRWGCMQSNQSNLYNGQSLSFCVYTTSDGRTIYNNAPSWGQGF	227	

```

RESULT 7
T10079
expansin S1 precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C:Accession: T10079
R:Sheehan, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh,
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi-
A:Reference number: Z14894; MUID:96016146; PMID:7568110
A:Accession: T10079
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-250 <SHC>
A:Cross-references: UNIPROT:Q39625, UNIPARC:UPI00000A29F, EMBL:U30382, NID:g1040874, PI
A:Experimental source: cultivar Burpee Pickler

```

C:Genetics:
A:Gene: EXP1
C:Function:
A:Description: mediates cell wall extension
F1-23/Domain: signal sequence #status predicted <A>
F1-24-350/Product: expansin #status predicted <WMT>

Query Match	63.8%	Score	895.5	DB 2	Length	250			
Best Local Similarity	65.9%	Fred.	No. 2.7e-69						
Matches	162	Conservative	30	Mismatches	49	Indels	5	Gaps	4
<hr/>									
QY	10	SLIGLCCTITTYAFSPSGMTNAHATFYGSDASGTWGAAGYGNLYATGYGTRTAALST	69						
Db	10	SLFLLPFFVFTFA-DYCGWQSGHATFYGGDASGTWGAAGYGNLYGQGYGTIVTALST	68						
QY	70	ALFNDGASGQCYKICDKYSDSRMCIKGRVVTYATATPCPNPALPNNNGMCNPLKX	129						
Db	69	ALFNNGLSCGACPEMTCT-TNDPKNCLPG-TIRATATNFCPPNPALPNNNGMCNPLQH	125						
QY	130	FDMAQPAWEKIGIYRGIVPVLFORVPCKKHGQVAFSVNGHDYELVLIISNVGAGSIQS	189						
Db	126	FDMAEPALQIAQYRAGIVPVSFRRVPCMKKGQVRFRTNGHSFNLVLITVWGAAGDVHS	185						
QY	190	VFIKSGKGMAMASRNNWGSNNQSNAYLNGSLSRVTTTDETFVFODIVVSMTPGQTF	249						
Db	186	VSIKSRGIMGWSRHMGMQNMOSNNYTLNGSLFOVTLISDRITLTATVNLVSMQFGQTY	245						
QY	250	SSPVQF 255							
Db	246	EGP-QF 250							

RESULT 8
 T09825
 expansin (clone pPrexp4) - loblolly pine (fragment)
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
 C:Accession: T09825
 R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A:Description: Expansins are conserved in conifers and expressed in response to exogenous
 A:Reference number: Z16866
 A:Accession: T09825
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1*232 <HT>
 A:Cross-references: UNIPROT:P93494; UNIPARC:UPI00000A2A2C; EMBL:U64892; NID:g1778102; P

Query Match	63.8%	Score 894.5	DB 2	Length 232
Best Local Similarity	69.0%	Pred. No. 3.1e-69		
Matches	158	Conservative 29	Mismatches 39	Indels 3
			Gaps 2	
QY	21	TYAFSPSMTNAHAHTFYGGSDASGTMGACCGYGLVATGYGTTAALSTALEFNDGASCGQ	80	
DB	2	TGAHGYYGMEGAHAHTFYGGSDASGTMGACCGYGLVATGYGTTAALSTALEFNDGLSGCA	61	
QY	81	CYKIIIDYKSSRNCIKGRSTVTATATFCPPNFALPNNNGCMCPPLKHPMAOPAMEKI	140	
DB	62	CYEMQCN--DDPQWCLPG-TVTITATINFCPPNNALPNDNGCMCPPLQHPMAEPALFKI	118	
QY	141	GIYRGAIYVPLFORPCKKHGTVFVSVNGRIFYELVILSNVGGASIOSVPIKSGSKTGM	200	
DB	119	AKYRGAIYPIIYTRVPCILRKGIIFVTYNGHSCFPLVILITNVGGADVHAIVSIKPRSGMQ	178	
QY	201	AMSRRMGSMQSNAYLNGQSLSPRVTTTGDSTRVPDIIVPVSWTGGTF	249	
DB	179	PMSRRMGQMSNSYINGQSLSPVTTSDGTTVSNVAVPMMQFGDTF	227	

RESULT 9
T50654
expansin EXP1 [imported] - Arabidopsis thaliana (Fragment)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 12:28:54 ; Search time 38 Seconds

(without alignments)
645,665 Million cell updates/sec

Title: US-10-660-499a-2

Perfect score: 1403

Sequence: 1 MGKIMLVGSLIGLCCFTT.....QDIVPVSWTFGGTFSSVPQF 255

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103.5	78.7	258	2 T10083	expansin S2 precur
2	1091	77.8	252	2 F86335	hypothetical prote
3	1039	74.1	261	2 T03737	expansin - rice
4	909.5	64.8	232	2 T09821	expansin (clone p
5	909.5	64.8	232	2 T09826	expansin (clone p
6	906.5	64.6	232	2 T09818	expansin (clone p
7	895.5	63.8	250	2 T10079	expansin S1 precu
8	894.5	63.8	232	2 T09825	expansin (clone p
9	890.5	63.5	237	2 T50654	expansin EXP1 (imp
10	879.5	62.7	251	2 T03298	expansin 2 - rice
11	876.5	62.5	258	2 C84444	expansin
12	874	62.3	255	2 T02010	expansin homolog T
13	863.5	61.5	255	2 T50656	expansin EXP2 (imp
14	862	61.4	253	2 F84831	probable expansin
15	857.5	61.1	258	2 T09786	expansin - upland
16	849.5	60.5	246	2 T04175	expansin - rice
17	843.5	60.1	262	2 T02530	probable expansin
18	834.5	59.5	261	2 T07630	expansin 1 - tomat
19	829.5	59.1	257	2 D84820	probable expansin
20	829.5	59.1	252	2 T50660	alpha-expansin 2 (
21	827	58.9	255	2 T03299	expansin 3 - rice
22	826.5	58.9	258	2 S53082	pollen allergen ho
23	823.5	58.7	257	2 T02727	probable expansin
24	821.5	58.6	260	2 T47689	expansin-like prot
25	820.5	58.5	259	2 T50653	expansin EXP6 (imp
26	816.5	58.2	257	2 T50658	expansin 9 (impor
27	816	58.2	260	2 T08016	probable expansin
28	804.5	57.3	255	2 T06573	expansin 18 - toma
29	804.5	57.3	255	2 T50655	expansin EXP5 (imp

30	792.5	56.5	264	2 T50659	alpha-expansin OSE
31	784.5	55.9	258	2 T48247	expansin-like prote
32	670.5	47.8	257	2 G96654	hypothetical prote
33	668.5	47.6	257	2 F86259	protein T12C24.10
34	605.5	43.2	160	2 T09871	expansin - upland
35	533	38.0	256	2 T05648	expansin homolog F
36	302.5	21.6	259	2 T50658	beta-expansin (imp
37	302.5	21.6	271	2 H84592	beta-expansin (imp
38	290.5	20.7	276	2 T09041	ciml protein homol
39	284.5	20.3	102	2 T09828	expansin (clone p
40	280	20.0	77	2 T09815	expansin (clone p
41	278.5	19.9	491	2 F96681	protein F1822.6 (l
42	274.5	19.6	277	2 S48032	ciml protein - soy
43	264	18.8	81	2 T09830	expansin (clone p
44	257	18.3	261	2 T04301	beta-expansin - ri
45	238.5	17.0	263	2 B37881	pollen allergen lo

ALIGNMENTS

RESULT 1
T10083
expansin S2 precursor - cucumber
C/Species: Cucumis sativus (cucumber)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 31-Dec-2004
C/Accession: T10083
R/Shcherban, T.Y.; Shi, J.; Duracko, D.M.; Gullitman, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A/Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi A/Reference number: Z14894; MUID:96016146; PMID:7568110
A/Accession: T10083
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-258 <SHC>
A/Cross-references: UNIPROT:Q39626; UNIPARC:UPI00000AB540; EMBL:U30460; NID:G1040876; P F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-258/Product: expansin #status predicted <MAT>
C/Function:
A/Gene: EXP2
C/Genetic:
A/Experimental source: cv. Burpee Pickler; hypocotyl
A/Description: induces cell wall extension in plants
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-258/Product: expansin #status predicted <MAT>
Query Match 78.7%; Score 1103.5; DB 2; Length 258;
Best local Similarity 81.2%; Pred. No. 4.5e-87;
Matches 195; Conservative 22; Mismatches 22; Indels 1; Gaps 1;
QY 17 FTTTAYSPSCWMAATFYGSDASGTMGACGYGNLYATGYGRTAALSTALFNDA 76
DB 18 FFLFVNAFTASGMAPAHATFYGBSDASGTMGACGYGNLYOTGYGRTAALSTALFNDA 77
QY 77 SCGQCYKIIICDYKSDSRMCIKGRSVVTATNCPFPALPNNNGMCNPLKHFDAOPA 136
DB 78 SCGQCFKIIICDYKIDRCIKASVITITATNCPFPALPNNNGMCNPLKHFDAOPA 137
QY 137 WEKIGIRGAGIYVLFQRPVCKKGGVRSVANGRDYFELVILSNVGSAGISIVPIKGR 196
DB 138 MKKIGIRGGIIPVLYQRVPCKKRGVRFVANGRODFELVILTNNGADIDSVSIKGR 197
QY 197 TGMMASTNMGSNMOSNAYLNGQISFRVTTTGGTRVFDIIVPVSWTFGGTFSSVPQF 255
DB 198 SSWTFPSHMGANNQSNYSYLNQGISFRVTTSDGVQVFNVNVPSMRFGQTFASKVQF 257
RESULT 2
F86335
hypothetical protein T20H2.4 (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2004
C/Accession: F86335
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

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Job time : 163 secs

QY		125	PLKHKFMDMAOPAMEKIIGIRGGIVLPFLFORVPCCKHGVRRSPRSDPYELVLISNVGGA	184
Dd		126	PRPHFDMAOPACENIGIRGGIVLPALYQRIPCVKKGVARFTTNGRYFELLMIISNVGGA	185
QY		185	GSIQSVEFIKSGSTGWMMASRNMGSNMOSNAYLNGSLSFFRVTTTDDGETRFODIVPVSWT	244
Dd		186	GSVGVSQIIGSGSNMTWTSERNWCAMNNGSNAYLNGGPLSFRTVTITTDGYTKFLNAISSNM	245
QY		245	FCQTSSPVQF 255	
Dd		246	FCQTYSSTINF 256	
RESULT 12				
ID	094KT5_MAIZE	PRT;	262 AA.	
AC	094KT5;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DN	Alpha-expansin 3 precursor.			
GN	Name=expa3;			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBT_TaxId=4577;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=21249159; PubMed=11351085; DOI=10.1104/pp.126.1.222;			
RA	Wu Y., Meeley R.B., Cosgrove D.J.;			
RT	"Analysis and expression of the alpha-expansin and beta-expansin gene families in maize."			
RL	Plant Physiol. 126:222-232(2001).			
RM	EMBL; AF332171; AAK56121.1; -; mRNA.			
DR	GO; GO:0005618; C:cell wall; IEA.			
DR	GO; GO:0005576; C:extracellular region; IEA.			
DR	GO; GO:0009664; P:cell wall organization and biogenesis (sens. . . ; IEA.			
DR	GO; GO:0016068; P:type I hypersensitivity; IEA.			
DR	InterPro; IPRO02963; Expansin.			
DR	InterPro; IPRO07112; Expan_endogl.			
DR	InterPro; IPRO07117; Expan_lo1_pi.			
DR	InterPro; IPRO05132; Lipoprotein_13.			
DR	Pfam; PF03330; DPBB_1; 1.			
DR	Pfam; PF01357; Pollen_allerg_1; 1.			
DR	PRINTS; PRO1226; EXPANSIN.			
DR	PRINTS; PRO1225; EXPANSINFAMILY.			
DR	ProDom; PD002179; Expan_lo1_pi C; 1.			
DR	PROSITE; PS50843; EXPANSIN CBD; 1.			
DR	PROSITE; PS50842; EXPANSIN_BG45; 1.			
KW	Signal.			
FT	SIGNAL. 1	Potential.		
FT	SEQUENCE 262 AA; 27775 MW; DDGCF0569DF63BF9 CRC64;			
Query Match 74.3%; Score 1043; DB 2; Length 262;				
Best Local Similarity 75.0%; Pred. No. 2 2e-81;				
Matches 186; Conservative 24; Mismatches 38; Indels 0; Gaps 0				
QY		8	LGLSLGLCCFTTTYVAFSFGSWTNAAHTFYGSSDAGSTMGCAGCYGNLYATGYGTRTAAL	67
Dd		14	IALLLAACLIMKEBAFCFSASGLINKAKATAFYGSGSDASTGMGAGCYGNLYATGYGTDAAL	73
QY		68	SYALFNNDGASCQCQCYTIIDYKSDSMWCIKGRSVTYTATNFQCPNPRLPNNNGMCNPP	127
Dd		74	SYALFNNDGASCQCCHRISCDYQADPFCTLRGISVTTTAINLCPPNALPNDDGMCNPPR	133
QY		128	KHFDMAOPAMEKIIGIRGGIVLPFLFORVPCCKHGVRRSPRSDPYELVLISNVGAGSI	187
Dd		134	QHFDMAEPMLKITIGIRGGIVLPVNYRVRPCVKKGVARFTTNGRYFELLVLISNVGGGSI	193
QY		188	GSVFIFKSGSTGWMMASRNMGSNMOSNAYLNGSLSFRVTTTDDGETRFODIVPVSWTFG	247

Db	194	Q5AS1GSGRTGMMASRIMGVNMOSNAYLNGOSISFOVTSDDGQTKTTPDVAPASMGFGQ	253
Qy	248	TFESPVOF	255
Db	254	TFATSQOF	261
RESULT 13			
ID	024208	ORYSA PRELIMINARY;	PRT, 261 AA.
AC	024208		
DT	01-JAN-1998	(TEMBLrel. 05, Created)	
DT	01-JUN-1998	(TEMBLrel. 06, Last sequence update)	
DT	10-MAY-2005	(TEMBLrel. 30, Last annotation update)	
DE	Expansin precursor (Alpha-expansin OSEXP1).		
GN	Name=RIEXA; Synonyms=EXPAL;		
OC	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehharctoidae; Oryzeae; Oryza.		
CC	NCBI_TaxID=4530;		
NP	[1]		
NP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Shoot;		
KX	CHLHINE=97480100; PubMed=938967; DOI=10.1105/epc.9.9.1661;		
RA	Cho H.T., Kende H.;		
RT	"Expression of expansin genes is correlated with growth in deepwater		
RT	ce.";		
RL	Plant Cell 9:1661-1671(1997).		
NP	[2]		
NP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Shoot;		
RA	Cho H.;		
RL	Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.		
NP	[3]		
NP	NUCLEOTIDE SEQUENCE.		
KX	CHLHINE=15151099; PubMed=1641069; DOI=10.1016/S1369-5286(00)00211-9;		
RA	Lee Y., Choi D., Kende H.;		
RT	"Expansins: ever-expanding numbers and functions.";		
RL	Curr. Opin. Plant Biol. 4:527-532(2001).		
NP	[4]		
NP	NUCLEOTIDE SEQUENCE.		
KX	MELINE=22315554; PubMed=12428004; DOI=10.1104/pp.008888;		
RA	Lee Y., Kende H.;		
RT	"Expression of alpha-expansin and expansin-like genes in deepwater		
RT	rice.";		
RL	Plant Physiol. 130:1396-1405(2002).		
DR	EMBL; Y07782; CAA69105.1; - mRNA.		
DR	EMBL; AF394543; AAL24479.1; -; Genomic_DNA.		
DR	PIR; T03737; T03737.		
DR	Gmane; 024208; -.		
DR	GO; GO:0005618; C:cell wall; IEA.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.		
DR	GO; GO:0016068; P:type I hyperosmoticity; IEA.		
DR	InterPro; IPR002963; Expansin.		
DR	InterPro; IPR007112; Expansin_endog1.		
DR	InterPro; IPR007118; Expansin_endog1.		
DR	InterPro; IPR007117; Expansin_endog1.		
DR	InterPro; IPR005132; Lipolectin_13.		
DR	Pfam; PF03330; DPBB_1; 1.		
DR	Pfam; PF01357; Pollen_allerg_1; 1.		
DR	PRINTS; PRO1226; EXPANSIN.		
DR	PRINTS; PRO1225; EXPANSIN_PAMLY.		
DR	PROSITE; PSS0843; EXPANSIN_CBD; 1.		
DR	PROSITE; PSS0842; EXPANSIN_EG45; 1.		
KW	Signal.		
FT	SIGNAL	1	18 Potential.
SQ	SEQUENCE	261 AA; 27748 MW; 941705D5617B6FF8 CRC64;	
Query Match		74.1%; Score 1039; DB 2; Length 261;	
Best Local Similarity		73.2%; Pred.No. 4.7e-81;	

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FT SIGNAL 1 22 Potential.
CHAIN 23 256 alpha-expansin.
SQ SEQUENCE 256 AA, 27754 MW, 688341755B0E0801 CRC64;

Query Match
Best Local Similarity 76.3%; Score 1070; DB 2; Length 256;
Matches 185; Conservative 27; Mismatches 39; Indels 0; Gaps 0;

QY 5 MLVLSLGLCCFTITTTAFSPSGMTNAAATFYGSDASGTMGACGYGNLYATGYGRT 64
DB 6 ILALGIFRIFCNHFPNANFSAAGSATAATFYGSDASGTMGACGYGNLYSTGYGNT 65
QY 65 AALSTALFNDGASCCQCYKICDYKSDSRWCIGRSVYTTATNFCPPNFPALPNNGWCN 124
DB 66 AALSTALFNDGASCCQCYKIMCDYNDPCKCRKGYTTTATNFCPPNFPALPNNGWCN 125
QY 125 PPLKHFDMQAQPAWEKIGYRGIIVPVLFGQVPCPKKHGVRFSVNGRDYELVLI 184
DB 126 PRPHFDMAQPAWENIGYRGIIVPVLQRIQPCVKKGVRFTINGRNYFELMISVGA 185
QY 185 GSIGSVFTKSGTKTGMMAMRNNGSNQSNAYLNGSLSTRVTTTDSGTRVFDIYVSWT 244
DB 186 GSIGSVFTKSGTKTGMMAMRNNGSNQSNAYLNGSLSTRVTTTDSGTRVFDIYVSWT 245
QY 245 FCQTFSSPVQF 255
DB 246 FCQTFSTSTINF 256

RESULT 10
Q9FY57_9LAMI PRELIMINARY; PRT; 257 AA.
ID Q9FY57_9LAMI PRELIMINARY; PRT; 257 AA.
AC Q9FY57;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-expansin 3.
OS Striga asiatica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Lamiales; Orobanchaceae; Buchneraeae; Striga.
OC NCBI_Taxid=4170;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Malley R.C., Lynn D.G.;
RT "Expansin Regulation in Parasitic Angiosperms: Marking Time in
RT Development."
RL Plant Cell 0:0-0(2000).
EMBL: AF291659; AAC01875.1; -; mRNA.
DR GO:GO:0005618; C:cell wall; IEA.
DR GO:GO:0005576; C:extracellular region; IEA.
DR GO:GO:0009664; P:cell wall organization and biogenesis (sens. .); IEA.
DR GO:GO:0006952; P:defense response; IEA.
DR InterPro: IPR002963; Expansin.
DR InterPro: IPR007112; Expan_endogl.
DR InterPro: IPR007118; Expan_lo1_pi.
DR InterPro: IPR007117; Expan_lo1_pi.
DR InterPro: IPR005132; Lipoprotein_13.
DR Pfam: PF03330; DPBB_1; 1.
DR Pfam: PF01357; Pollen_allerg_1; 1.
DR PRINTS: PRO1226; EXPANSIN.
DR PRINTS: PRO1225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Expan_lo1_pi.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 257 AA, 27751 MW, 349826B0326D93C4 CRC64;

Query Match
Best Local Similarity 76.0%; Score 1066; DB 2; Length 257;
Matches 188; Conservative 31; Mismatches 36; Indels 2; Gaps 1;

QY 1 MCKIMLVLSLGLCCFTITTTAFSPSGMTNAAATFYGSDASGTMGACGYGNLYAT 58
DB 6 ILALGIFRIFCNHFPNANFSAAGSATAATFYGSDASGTMGACGYGNLYSTGYGNT 65

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DB 1 MCKNRSPLIYLVACFCLLIINANGFTASGWTQAATFYGSDASGTMGACGYGNLYST 60
QY 59 GYRTTALSTALFNDGASCCQCYKICDYKSDSRWCIGRSVYTTATNFCPPNFPALPN 118
DB 61 GYRTTALSTALFNDGASCCQCYKIMCDYNDPCKCRKGYTTTATNFCPPNFPALPN 120
QY 119 NGCMNPPPLKHFDMQAQPAWEKIGYRGIIVPVLFGQVPCPKKHGVRFSVNGRDYELVLI 178
DB 121 NGCMNPPRQHFDMQAQPAWQKIAIKGGIIVPVLQYQVPCPKKHGVRFTINGRNYFELVLY 180
QY 179 SNVGAAGSIQSVFTKSGTKTGMMAMRNNGSNQSNAYLNGSLSTRVTTTDSGTRVFDI 238
DB 181 SNVGAAGSVRSYKIGSKTDWMSRNQALMQSNLYNGSLSPWVTTSDCSKNSLSLV 240
QY 239 VPSWTFQGTSSPVQF 255
DB 241 VPSNMAFGQTFSSGVQF 257

RESULT 11
Q9ZP38_TOBAC PRELIMINARY; PRT; 256 AA.
ID Q9ZP38_TOBAC PRELIMINARY; PRT; 256 AA.
AC Q9ZP38;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-expansin precursor.
GN Name=Nt-EXPA2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_Taxid=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Link B.M., Cosgrove D.J.;
RX MEDLINE=99026292; PubMed=9808735; DOI=10.1104/pp.118.3.907;
RT "Acid-growth response and alpha-expansins in suspension cultures of
RT bright yellow 2 tobacco."
RL Plant Physiol. 118:907-916(1998).
EMBL: AF049351; AAC96078.1; -; mRNA.
DR GO:GO:0005618; C:cell wall; IEA.
DR GO:GO:0005576; C:extracellular region; IEA.
DR GO:GO:0009664; P:cell wall organization and biogenesis (sens. .); IEA.
DR GO:GO:0006952; P:defense response; IEA.
DR InterPro: IPR002963; Expansin.
DR InterPro: IPR007112; Expan_endogl.
DR InterPro: IPR007118; Expan_lo1_pi.
DR InterPro: IPR007117; Expan_lo1_pi.
DR InterPro: IPR005132; Lipoprotein_13.
DR Pfam: PF03330; DPBB_1; 1.
DR Pfam: PF01357; Pollen_allerg_1; 1.
DR PRINTS: PRO1226; EXPANSIN.
DR PRINTS: PRO1225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Expan_lo1_pi.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 24 Potential.
FT CHAIN 25 256 alpha-expansin.
SQ SEQUENCE 256 AA, 27604 MW, A7478B9130C0416D CRC64;

Query Match
Best Local Similarity 75.0%; Score 1052; DB 2; Length 256;
Matches 182; Conservative 28; Mismatches 41; Indels 0; Gaps 0;

QY 5 MLVLSLGLCCFTITTTAFSPSGMTNAAATFYGSDASGTMGACGYGNLYATGYGRT 64
DB 6 ILALGIFRIFCNHFPNANFSAAGSATAATFYGSDASGTMGACGYGNLYSTGYGNT 65
QY 65 AALSTALFNDGASCCQCYKICDYKSDSRWCIGRSVYTTATNFCPPNFPALPNNGWCN 124
DB 66 AALSTALFNDGASCCQCYKIMCDYNDPCKCRKGYTTTATNFCPPNFPALPNNGWCN 125

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DR InterPro; IPR007118; Expan_LoI_PI.
 DR InterPro; IPR007117; Expan_LoI_PI_C.
 DR InterPro; IPR005132; Lipoprotein_13.
 DR Pfam; PF03330; DPBB_1; 1.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01226; EXPANSIN.
 DR PRINTS; PR01225; EXPANSIN.FAMILY.
 DR ProDom; PD002179; Expan_LoI_PI_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 256 AA; 27648 MW; 76CAE091CD0F1CB0 CRC64;

Query Match 77.7%; Score 1089.5; DB 2; Length 256;
 Best Local Similarity 74.6%; Pred. No. 2.1e-85;
 Matches 191; Conservative 32; Mismatches 32; Indels 1; Gaps 1;

QY 1 MKKI-MLVVSLIGLCCFTITTYAFSPSGMTNHAATFYGGSDASGTMGACGYNLYATG 59
 DB 1 MAKICIALGFIPLGLNIILSNANAFSASGMSHAATFYGGSDASGTMGACGYNLYSTG 60
 QY 60 YGTRTALSTALFNDGASCGQCYKIICDYKSDSRWCIKGRSVTVTATNFCPPNFALPNN 119
 DB 61 YGTRTALSTALFNDGASCGQCYKIICDYKSDSRWCIKGRSVTVTATNFCPPNFALPNN 120
 QY 120 GGMCPPLKHPMAQPAWEKIGYRGIVPVLPQRPCKKGGVRSVNGRDYFELVLIS 179
 DB 121 GGMCPPRPHFMAQPAWEHIGYRGIVPVLPQRPCKKGGVRSVNGRDYFELVLIS 180
 QY 180 NVGAGSISQSVFIKSGKTGMAMSRNMGSNWQSNAYLNGOSLSFRVTTTGGTFRVQDVI 239
 DB 181 NVGAGSVSVQIKSGRTNMAMSRNMGANWQSNAYLNGOSLSFRVTTTGGTFRVQDVI 240
 QY 240 PVSMTFGQTSSPVQF 255
 DB 241 SSMWGQGYSSSMNF 256

RESULT 8
 Q9ZP37_TOBAC PRELIMINARY; PRT; 257 AA.

ID Q9ZP37_TOBAC PRELIMINARY; PRT; 257 AA.
 AC Q9ZP37_
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-expansin precursor.
 GN Name=Nt-ExpA3;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99026292; PubMed=9808735; DOI=10.1104/pp.118.3.907;
 RA Link B.M., Cosgrove D.J.;
 RT "Acid-growth response and alpha-expansins in suspension cultures of
 RT bright yellow 2 tobacco.";
 RL Plant Physiol. 118:907-916 (1998).
 DR EMBL; AF049352; AAC96079.1; -; mRNA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR002963; Expansin.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_LoI_PI.
 DR InterPro; IPR007117; Expan_LoI_PI_C.
 DR InterPro; IPR000583; GATase_2.
 DR InterPro; IPR005132; Lipoprotein_13.
 DR Pfam; PF03330; DPBB_1; 1.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01226; EXPANSIN.
 DR PRINTS; PR01225; EXPANSIN.FAMILY.

DR ProDom; PD002179; Expan_LoI_PI_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 257 AA; 27917 MW; 1E09E2B148BD56 CRC64;

Query Match 77.5%; Score 1087; DB 2; Length 257;
 Best Local Similarity 75.3%; Pred. No. 3.5e-85;
 Matches 189; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 5 MLVSLIGLCCFTITTYAFSPSGMTNHAATFYGGSDASGTMGACGYNLYATGTRT 64
 DB 6 IIALGFIILFFSIFPRNANFTASGWRATFYGGSDASGTMGACGYNLYSTGYTGS 65
 QY 65 AALSTALFNDGASCGQCYKIICDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGWGN 124
 DB 66 AALSTALFNDGASCGQCYKIICDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGWGN 125
 QY 125 PLKHPDMAQPAWEKIGYRGIVPVLPQRPCKKGGVRSVNGRDYFELVLISNVGA 184
 DB 126 PRQHPDMAQPAWEKIGYRGIVPVLPQRPCKKGGVRSVNGRDYFELVLISNVGA 185
 QY 185 GSISQSVFIKSGKTGMAMSRNMGSNWQSNAYLNGOSLSFRVTTTGGTFRVQDVI 244
 DB 186 GSVRSVQIKSGRTNMAMSRNMGANWQSNAYLNGOSLSFRVTTTGGTFRVQDVI 245
 QY 245 FGQTFSSPVQF 255
 DB 246 FGQTFSSPTQF 256

RESULT 9
 Q9ZP39_TOBAC PRELIMINARY; PRT; 256 AA.

ID Q9ZP39_TOBAC PRELIMINARY; PRT; 256 AA.
 AC Q9ZP39;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-expansin precursor.
 GN Name=Nt-ExpA1;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99026292; PubMed=9808735; DOI=10.1104/pp.118.3.907;
 RA Link B.M., Cosgrove D.J.;
 RT "Acid-growth response and alpha-expansins in suspension cultures of
 RT bright yellow 2 tobacco.";
 RL Plant Physiol. 118:907-916 (1998).
 DR EMBL; AF049350; AAC96077.1; -; mRNA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR002963; Expansin.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_LoI_PI.
 DR InterPro; IPR007117; Expan_LoI_PI_C.
 DR InterPro; IPR005132; Lipoprotein_13.
 DR Pfam; PF03330; DPBB_1; 1.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01226; EXPANSIN.
 DR PRINTS; PR01225; EXPANSIN.FAMILY.
 DR ProDom; PD002179; Expan_LoI_PI_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 KW Signal.

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_Taxid=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;
 RA MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
 RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Alcafi J.R., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chao A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malet R., Marshall A.,
 RA Miltner J., Miranda W., Nguyen M., Niemman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana."
 RL Nature 408:816-820(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22354850; PubMed=14593172; DOI=10.1126/science.1088305;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Souvick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlén-Nemmann G., Liu S.X., Lam B., Sakano H., Mu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansel Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsu V.W., Iida K., Kamei M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamuya A., Meyers C., Nakajima M., Natsumaki M., Seki M., Sakurai T.,
 RA Satou M., Tamez R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome."
 RL Science 302:842-846(2003).
 RN [3]
 RP TISSUE SPECIFICITY.
 RA Durachko D.M., Cosgrove D.J.,
 RT "Expression patterns for selective expansin genes in Arabidopsis."
 RL (in) Proceedings of Plant Biology '99: The annual meeting of the
 RL American Society of Plant Physiologists, abstract#56, Baltimore
 RL (1999).
 CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
 CC disrupting noncovalent bonding between cellulose microfibrils and
 CC matrix glucans. No enzymatic activity has been found (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
 CC -1- TISSUE SPECIFICITY: Expressed in the leaf, but not in the
 CC epidermis or in the vascular bundles.
 CC -1- SIMILARITY: Belongs to the expansin family.
 CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
 CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
 CC -1- DATABASE: NAME=EXPANSIN homepage;
 CC WWW="http://www.bio.psu.edu/expansins/".
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC DR EMBL: AC022472; AAF79895.1; -; Genomic_DNA.
 CC DR EMBL: AF332436; AAG48799.1; -; mRNA.

DR PIR: P86335; P86335.
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_Lo1_pi.
 DR InterPro: IPR007117; Expan_Lo1_pi_C.
 DR InterPro: IPR002963; Expanin.
 DR InterPro: IPR005132; R1PA.
 DR Pfam: PF03330; DPBB.1; 1.
 DR Pfam: PF01357; Pollen_allerg_1; 1.
 DR PRINTS: PR01226; EXPANSIN.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_Lo1_pi_C; 1.
 DR PROSITE: PS50843; EXPANSIN CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 DR Cell wall; Multigene family; Signal.
 KW SIGNAL.
 FT CHAIN 1 20 Potential.
 FT DOMAIN 21 252 Alpha-expansin 11.
 FT DOMAIN 169 248 Expansin-like EG45.
 FT DOMAIN 169 248 Expansin-like CBD.
 SQ SEQUENCE 252 AA; 26761 MW; 9CE86DA49BEA31B CRC64;
 Query Match 77.8%; Score 1091; DB 1; Length 252;
 Best Local Similarity 78.6%; Pred. No. 1.6e-85;
 Matches 195; Conservative 20; Mismatches 33; Indels 0; Gaps 0;
 QY 8 LGSILGLCCFTTITTYTAFSPSGMTNAAATFYGSDASGTMGACGYNLYATGYCTRTAL 67
 DB 5 IAGLVLAALFVAVDAFRPSGLTNGHATFYGSDASGTMGACGVDLYSAGYGTMTAL 64
 QY 68 STALFNIDGASCGGCKYITCDYKSDSRWCTKGSVYVATNFPCCPPALPNNNGMCPPL 127
 DB 65 STALFNIDGASCGECRITCDHADSRWCLKGSVITATNFPCCPPALPNNNGMCPPL 124
 QY 128 KIFDAAQAPMEKIGYRGIVLFFORVPCCKHGVRSVNGRDYFELVLSNVGAGSI 187
 DB 125 KIFDAAQAPMEKIGYRGIVLFFORVPCCKHGVRSVNGRDYFELVLSNVGAGSI 184
 QY 188 QGVFKGSKTGMAMSRNMGWSNAYINGSLSPRTVTGTEFRVFDIPIVSTPQQ 247
 DB 185 KSVISKSGXTGTLAMSRMGWNSNAYIDGALSFTITTDGATRVFNVVSSWSFQQ 244
 QY 248 TFSPPVQF 255
 DB 245 IYSSNVQF 252
 RESULT 7
 ID 08S346 CAPAN PRT; 256 AA.
 AC 08S346;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Putative expansin.
 GN Name=upa7a;
 OS Capsicum annuum (Bell pepper).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; Lamiales; Solanales; Solanaceae; Capsicum.
 OC NCBI_Taxid=4072;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22113994; PubMed=12118879;
 RA Marois E., Van den Ackereken G., Bonas U.,
 RT "The xanthomonas type III effector protein in AvrBs3 modulates plant gene
 RT expression and induces cell hypertrophy in the susceptible host."
 RL Mol. Plant Microbe Interact. 15:637-646 (2002).
 DR EMBL: AF492631; AAM12783.1; -; mRNA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
 DR GO: GO:0009552; P:defense response; IEA.
 DR InterPro: IPR002963; Expansin.
 DR InterPro: IPR007112; Expan_endogl.

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06KEZ3 LYCES
ID 06KEZ3 LYCES PRELIMINARY; PRT; 257 AA.
AC 06KEZ3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Expansion1 precursor.
GN Name=expi1;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxId=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vogler H., Mandel T.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; A550646; CAD90260.1; -; mRNA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR002963; Expansin.
DR InterPro; IPR007112; Expansin.
DR InterPro; IPR007118; Expansin.
DR InterPro; IPR007117; Expansin.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPB8_1; 1.
DR Pfam; PF01357; Pollen allergen_1; 1.
DR PRINTS; PR01226; EXPANSIN.
DR PRODOM; PD002179; Expansin.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Signal.
FT SIGNAL 1 25 potential.
FT CHAIN 26 257 expansin1.
SQ SEQUENCE 257 AA; 27716 MW; 0CCC051525D62E CRC64;

Query Match 78.0%; Score 1094; DB 2; Length 257;
Best Local Similarity 75.1%; Pred. No. 8.8e-86;
Matches 133; Conservative 29; Mismatches 33; Indels 2; Gaps 2;

QY 1 MGKI-MLVIGSLGLCCFTITT-YAFSPSGMTNAHATFYGSDASGTMGACGYGNLYAT 58
DB 1 MAKIIGLTGFIKVFPCNIIIVSTANAFSAGMSAHATFYGSDASGTMGACGYGNLYST 60
QY 59 GYGTIRNALSTALFNDGASGCGCYKICDYKSDSRKICRSYTVTATNFCPPNFPALPN 118
DB 61 GYGTIRNALSTALFNDGASGCGCYKICDYKSDSRKICRSYTVTATNFCPPNFPALPN 120
QY 119 NGMGNPPLKHPMAOPAMEKIGIRGIVPVLFORVPCCKGIVRFSVNGRDYFELVLI 178
DB 121 NGMGNPPLKHPMAOPAMEKIGIRGIVPVMOKIPCYKKGAVRFTINGRIYFELMI 180
QY 179 SNVGAGSIQSVFIKSGKTGMAMSRNWSNWSNAYLNGQSLSPRYTTTDETRVFODI 238
DB 181 SNVGAGSIQSVFIKSGRTMTMARMWGANWQSNFLNGQSLSPKVTTSIDGYTKIFLNV 240
QY 239 VPVSWTFGQTFSSPVQF 255
DB 241 ASNMRFQGTYSSTINF 257

RESULT 5
QBLG16 ARATH PRELIMINARY; PRT; 252 AA.
ID QBLG16 ARATH PRELIMINARY; PRT; 252 AA.
AC QBLG16;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Alpha-expansin 11 (At-Expi1) (Ath-ExpAlp1a-1.14).
OS Arabidopsis thaliana (Mouse-ear cress).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Haas B.U., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY084514; AAM61082.1; -; mRNA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR InterPro; IPR002963; Expansin.
DR InterPro; IPR007112; Expansin.
DR InterPro; IPR007118; Expansin.
DR InterPro; IPR007117; Expansin.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPB8_1; 1.
DR Pfam; PF01357; Pollen allergen_1; 1.
DR PRINTS; PR01226; EXPANSIN.
DR PRODOM; PD002179; Expansin.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 252 AA; 26733 MW; 0C406A7BE61D49BC CRC64;

Query Match 77.8%; Score 1092; DB 2; Length 252;
Best Local Similarity 78.6%; Pred. No. 1.3e-85;
Matches 195; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 8 LGSILGLCCFTITTTT-YAFSPSGMTNAHATFYGSDASGTMGACGYGNLYATGYGTAL 67
DB 5 LAGLATLALFLAVDAFKPSGLTNGHATFYGSDASGTMGACGYGDDYISAGGTMTAL 64
QY 68 STALFNDGASGCGCYKICDYKSDSRKICRSYTVTATNFCPPNFPALPNNGMGNPPL 127
DB 65 STALFNDGASGCGCYKICDYKSDSRKICRSYTVTATNFCPPNFPALPNNGMGNPPL 124
QY 128 KHPDMAOPAMEKIGIRGIVPVLFORVPCCKGIVRFSVNGRDYFELVLIISVGAGSI 187
DB 125 KHPDMAOPAMEKIGIRGIVPVLFORVPCCKGIVRFSVNGRDYFELVLIISVGAGSI 184
QY 188 OSVFIKSGKTGMAMSRNWSNWSNAYLNGQSLSPRYTTTDETRVFODIIVSWTFQ 247
DB 185 KSVISIGSKTGMAMSRNWSNWSNAYLNGQSLSPRYTTTDETRVFODIIVSWTFQ 244
QY 248 TFSPPVQF 255
DB 245 IYSSNVQF 252

RESULT 6
EXPI1 ARATH STANDARD; PRT; 252 AA.
ID EXPI1 ARATH STANDARD; PRT; 252 AA.
AC 09LNU3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alpha-expansin 11 precursor (AtEXPA11) (At-EXPI1) (Ath-
DE ExpAlp1a-1.14).
GN Name=EXPI1; Synonyms=EXPI1; OrderedLocuNames=Atlg20190;
GN ORFNames=T20H2.4, T20H2.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Db      61 GTRTALSTALFNDGASCGQCYKIIIDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNG 120
Qy      121 GWCNPLKHFDMAGPAMEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 180
Db      121 GWCNPLKHFDMAGPAMEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 180
Qy      181 VGGAGSIOSVFIKSGKTGMAMSRMGSNMGSNAYLNGSLSPRVTTTDTGETRVFDIYP 240
Db      181 VGGAGSIOSVFIKSGKTGMAMSRMGSNMGSNAYLNGSLSPRVTTTDTGETRVFDIYP 240
Qy      241 VSMTFQGFSSPVQF 255
Db      241 VSMTFQGFSSPVQF 255

RESULT 2
Q9FVH0_LYCES PRELIMINARY; PRT; 257 AA.
ID      09FVH0;
AC      09FVH0;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DE      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Name=EXPASIN;
OS      Lycopersicon esculentum (Tomato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC      asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX      NCBI_TaxID=4081;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=20532800; PubMed=11080302; DOI=10.1104/pp.124.3.1265;
RX      Chen F., Bradford K.U.;
RT      "Expression of an expansin is associated with endosperm weakening
RT      during tomato seed germination."
RL      Plant Physiol. 124:1265-1274(2000).
DR      EMBL; AF184232; AAC32920.1; -; mRNA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0005576; C:extracellular region; IEA.
DR      GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR      GO; GO:0006952; P:defense response; IEA.
DR      InterPro; IPR002963; Expansin.
DR      InterPro; IPR007112; Expan_endogl.
DR      InterPro; IPR007118; Expan_lo1_pi_c.
DR      InterPro; IPR007117; Expan_lo1_pi_c.
DR      InterPro; IPR005132; Lipoprotein_13.
DR      Pfam; PF03330; DPBB_1; 1.
DR      Pfam; PF01357; Pollen allerg_1; 1.
DR      PRINTS; PR01226; EXPANSIN.
DR      PRINTS; PR01225; EXPANSINFAMILY.
DR      PRODOM; PD002179; Expan_lo1_pi_c; 1.
DR      PROSITE; PS50843; EXPANSIN_CBD; 1.
DR      PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ      SEQUENCE 257 AA; 27597 MW; C31FDC68BAD3760D CRC64;

Query Match 79.2%; Score 1110.5; DB 2; Length 257;
Best Local Similarity 77.1%; Pred. No. 3.4e-87;
Matches 195; Conservative 28; Mismatches 29; Indels 1; Gaps 1;

Qy      4 IMLVLSLIGLCTCFITTTVAFS--PSGWTNAHATFYGSDASGTMGACGYNLYATGYGT 62
Db      5 VNLALFTLIGLCTCFSSANGFSADSGWTSNAHTFYGGADSGTMGACGYNLYATGYGT 64

Qy      63 RTAALSTALFNDGASCGQCYKIIIDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGW 122
Db      65 RTAALSTALFNDGASCGQCYKIIIDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGW 124

Qy      123 CNPPLKHFDMAGPAMEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 182
Db      125 CNPPLKHFDMAGPAMEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 184

Qy      183 GAGSIOSVFIKSGKTGMAMSRMGSNMGSNAYLNGSLSPRVTTTDTGETRVFDIYPVS 242
Db      183 GAGSIOSVFIKSGKTGMAMSRMGSNMGSNAYLNGSLSPRVTTTDTGETRVFDIYPVS 242
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Db      185 GAGSVESVQIGSNTNMTLMSRWGASWQSNAYLNGSLSPRVTTSDGVTKFLNIIVPS 244
Qy      243 WTFQGFSSPVQF 255
Db      243 WTFQGFSSPVQF 255

RESULT 3
Q39626_CUCSA PRELIMINARY; PRT; 258 AA.
ID      Q39626_CUCSA
AC      Q39626;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Expansin S2.
DE      Name=Cu-EXPA2;
OS      Cucumis sativus (Cucumber).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC      rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX      NCBI_TaxID=3659;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=Surpee Pickler; TISSUE=Hypocotyl;
RX      MEDLINE=96016146; PubMed=7568110;
RX      Shecheran T.Y., Shi J., Durachko D.M., Gullinan M.J.,
RX      McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT      "Molecular cloning and sequence analysis of expansins - a highly
RT      conserved, multigene family of proteins that mediate cell wall
RT      extension in plants."
RL      Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
DR      EMBL; U30460; AA837749.1; -; mRNA.
DR      PIR; T10083; T10083.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0005576; C:extracellular region; IEA.
DR      GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR      InterPro; IPR002963; Expansin.
DR      InterPro; IPR007112; Expan_endogl.
DR      InterPro; IPR007118; Expan_lo1_pi_c.
DR      InterPro; IPR005132; Lipoprotein_13.
DR      Pfam; PF03330; DPBB_1; 1.
DR      Pfam; PF01357; Pollen allerg_1; 1.
DR      PRINTS; PR01226; EXPANSIN.
DR      PRINTS; PR01225; EXPANSINFAMILY.
DR      PRODOM; PD002179; Expan_lo1_pi_c; 1.
DR      PROSITE; PS50843; EXPANSIN_CBD; 1.
DR      PROSITE; PS50842; EXPANSIN_EG45; 1.
FT      CHAIN 25
FT      EXPANSIN S2.
SQ      SEQUENCE 258 AA; 28186 MW; A7FE19DCFBBD651 CRC64;

Query Match 78.7%; Score 1103.5; DB 2; Length 258;
Best Local Similarity 81.2%; Pred. No. 1.3e-86;
Matches 195; Conservative 22; Mismatches 22; Indels 1; Gaps 1;

Qy      17 FTITTAAPSFGWTNAHATFYGSDASGTMGACGYNLYATGYGTRTALSTALFNDGA 76
Db      18 FFLVNAALFASGAPAHATFYGESDSASGTMGACGYNLYATGYGTRTALSTALFNDGA 77

Qy      77 SCGQCYKIIIDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGWCNPLKHFDMAGP 136
Db      78 SCGQCYKIIIDYKSDSRWCIKGRSVTVTATNFCPPNFALPNNNGWCNPLKHFDMAGP 137

Qy      137 WKEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 196
Db      138 WKEKIGIRGGIVPVLFQVPCCKGGVRSVNGRDVFEVLISN 197

Qy      197 -TGMAMSRMGSNMGSNAYLNGSLSPRVTTTDTGETRVFDIYPVS 255
Db      198 SSMWTMSNMGMAMSGNSNAYLNGSLSPRVTTSDGVQVFNWVPSMFGQTFASKVQF 257

RESULT 4
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 12:27:53 ; Search time 161 Seconds

(without alignments)
1117.452 Million cell updates/sec

Title: US-10-660-499a-2

Perfect score: 1403

Sequence: 1 MGKIMLVLSLIGLCCFTIT.....QDIVPVSMTGTFSPVQF 255

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	100.0	255	2	Q8GZD3_SOYBN
2	1110.5	79.2	257	2	Q9FVH0_LYCHS
3	1103.5	78.7	258	2	Q39626_CUCSA
4	1094	78.0	257	2	Q6KEZ3_LYCHS
5	1093	77.8	252	2	Q8LGL6_ARATH
6	1091	77.8	252	1	EXPI1_ARATH
7	1089.5	77.7	256	2	Q8S346_CAPAN
8	1087	77.5	257	2	Q9ZP37_TOBAC
9	1070	76.3	256	2	Q9FVS7_GLAMI
10	1066	75.0	257	2	Q9ZP39_TOBAC
11	1062	75.0	256	2	Q9ZP38_TOBAC
12	1043	74.3	252	2	Q94RT5_MAZE
13	1039	74.1	261	2	Q24208_ORYSA
14	1039	74.1	261	2	Q7XWU8_ORYSA
15	1033.5	73.7	267	2	Q4LET2_GLITI
16	1002	71.4	262	2	Q5ETP6_WHEAT
17	987	70.3	263	2	Q8S828_ORYSA
18	987	70.3	263	2	Q5Z8N7_ORYSA
19	977	69.6	235	2	Q4PR39_ORYSA
20	971.5	69.2	262	2	Q94618_ORYSA
21	971.5	69.2	262	2	Q6ERV0_ORYSA
22	965.5	68.8	262	2	Q4PRS2_ORYSA
23	937	66.8	268	2	Q4LES9_GLITI
24	936.5	66.7	250	2	Q7G6Z2_ORYSA
25	936.5	66.7	250	2	Q94619_ORYSA
26	930	66.3	252	2	Q84136_MIRJA
27	928.5	66.2	261	2	Q4PR43_ORYSA
28	928.5	66.2	267	2	Q946H9_ORYSA
29	920	65.6	267	2	Q6ERU4_ORYSA
30	920	65.6	268	2	Q8LMP7_ORYSA
31	920	65.6	260	2	Q94616_ORYSA

32	920	65.6	262	2	Q94617_ORYSA	Q94617 oryza sativ
33	920	65.6	262	2	Q6ERU6_ORYSA	Q6ERU6 oryza sativ
34	920	65.6	274	2	Q4PR44_ORYSA	Q4PR44 oryza sativ
35	920	65.6	280	2	Q6ERU0_ORYSA	Q6ERU0 oryza sativ
36	918.5	65.5	253	2	Q9FY31_FESPR	Q9FY31 festuca pra
37	916	65.3	252	2	Q4PRS1_ORYSA	Q4PRS1 oryza sativ
38	914.5	65.2	278	2	Q6ERU5_ORYSA	Q6ERU5 oryza sativ
39	914	65.1	248	2	Q8LSG5_CICAR	Q8LSG5 cicar ariet
40	912.5	65.0	253	2	Q9SMY1_PINTA	Q9SMY1 pinus taeda
41	909.5	64.8	232	2	Q93493_PINTA	Q93493 pinus taeda
42	909.5	64.8	232	2	P93495_PINTA	P93495 pinus taeda
43	907	64.6	249	2	Q6TSH5_PROSI	Q6TSH5 populus tre
44	906.5	64.6	232	2	P93492_PINTA	P93492 pinus taeda
45	906.5	64.6	278	2	Q946H8_ORYSA	Q946H8 oryza sativ

ALIGNMENTS

RESULT 1	Q8GZD3_SOYBN	PRELIMINARY;	PRT;	255 AA.
ID	Q8GZD3_SOYBN	PRELIMINARY;	PRT;	255 AA.
AC	Q8GZD3;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Expansin.			
GN	Name=EXP1;			
OS	Glycine max (Soybean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	Rosales; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;			
OC	Glycine.			
OX	NCBI_TaxID=3847;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22531768; PubMed=12644651; DOI=10.1104/pp.009902;			
RA	Lee D.K., Ann J.H., Song S.K., Choi Y.D., Lee U.S.;			
RT	"Expression of an expansin gene is correlated with root elongation in			
RT	soybean."			
RL	Plant Physiol. 131:985-997(2003).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Lee D.-K., Ahn J.H., Choi Y.D., Lee U.S.;			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF516879; AA01598.1; -; mRNA.			
DR	GO; GO:0005618; C:cell wall; IEA.			
DR	GO; GO:000576; C:extracellular region; IEA.			
DR	GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.			
DR	InterPro; IPR002963; Expansin.			
DR	InterPro; IPR007112; Expan_endogl.			
DR	InterPro; IPR007118; Expan_lo1_pi.			
DR	InterPro; IPR005132; Lipoprotein_13.			
DR	Pfam; PF03330; DPEB_1; 1.			
DR	Pfam; PF01357; Pollen_allerg_1; 1.			
DR	PRINTS; PRO1225; EXPANSINFAMLY.			
DR	PRINTS; PRO1225; EXPANSINFAMLY.			
DR	ProDom; PD002179; Expan_lo1_pi_C; 1.			
DR	PROSITE; PSS0843; EXPANSIN_CBD; 1.			
DR	PROSITE; PSS0842; EXPANSIN_EG45; 1.			
SQ	SEQUENCE 255 AA; 27566 MW; 35831698B7756151 CRC64;			
Query Match	100.0%; Score 1403; DB 2; Length 255;			
Best Local Similarity	100.0%; Pred. No. 2.5e-112; Indels 0; Gaps 0;			
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MGKIMLVLSLIGLCCFTITTYAFSPSGWTNHAATFGSGDSAGTNGACGYGNTLYATGY 60			
DB	1 MGKIMLVLSLIGLCCFTITTYAFSPSGWTNHAATFGSGDSAGTNGACGYGNTLYATGY 60			
QY	61 GTTAAALSTALFNDGASGCGCTKIITDYKSDSWCKIGASVVTATNFCPPNPALENNNG 120			

QY 208 SNMOSNAYLNGQSLSPFRVTTTDDGETRVFODIVPVSWTFEGQTF 250
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 181 QNMOSNYLNGQSLSPFRVTTSDQITVSNMKNANAGMSFGQTF 223

RESULT 11

US-09-092-160-7
; Sequence 7, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullittan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cucumber
; OTHER INFORMATION: expansin
US-09-092-160-7

Query Match 62.7%; Score 879; DB 2; Length 227;
Best Local Similarity 67.5%; Pred. No. 1.6e-80;
Matches 154; Conservative 30; Mismatches 40; Indels 4; Gaps 3;

QY 28 GWTNAATFYGGSDASGTWGCAGYGNLYATGYGTRTALSTALFNDGASCGCYKIIDY 87
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 4 GWSGHAATFYGGSDASGTWGCAGYGNLYATGYGTRTALSTALFNDGASCGCYKIIDY 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 88 YKDSRWCICGRSVTYTATNFCPPNFPALPNNNGCMCPPLKHPDMAQPAHEKIGIYRGAI 147
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 63 -TNDPKWCLPG-TIRYTAIIFCPNFPALPNDGCMCPPLKHPDMAQPAHEKIGIYRGAI 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 148 VPVLPORVPCKKHGQVFSVNGRDYFELVLSNVGAGSIOVSFIKSKTGMAMSRNMG 207
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 121 VPVSPRRVPCMKKGQVRFITNGHSYFNLVLTNVGAGDVHVSIIKSRIGQMSNRNMG 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 208 SNMOSNAYLNGQSLSPFRVTTTDDGETRVFODIVPVSWTFEGQTFSSPVDF 255
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 181 QNMOSNYLNGQSLSPFRVTTSDQITVSNMKNANAGMSFGQTF 227

RESULT 12
US-09-112-498A-11
; Sequence 11, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
; TITLE OF INVENTION: SWOLLENINS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-112-498A-11

Query Match 62.0%; Score 870.5; DB 2; Length 233;
Best Local Similarity 67.9%; Pred. No. 1.2e-79;
Matches 150; Conservative 29; Mismatches 39; Indels 3; Gaps 2;

QY 29 WTNAAATFYGGSDASGTWGCAGYGNLYATGYGTRTALSTALFNDGASCGCYKIIDY 88
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 11 WGSAAATFYGGSDASGTWGCAGYGNLYATGYGTRTALSTALFNDGASCGCYKIIDY 69
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 89 KPSRWCICGRSVTYTATNFCPPNFPALPNNNGCMCPPLKHPDMAQPAHEKIGIYRGAI 148
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 70 -NDQWCLPG-STYVTAIIFCPNFPALPNDGCMCPPLKHPDMAQPAHEKIGIYRGAI 127
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 149 VPVLPORVPCKKHGQVFSVNGRDYFELVLSNVGAGSIOVSFIKSKTGMAMSRNMG 208
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 128 VPVSPRRVPCMKKGQVRFITNGHSYFNLVLTNVGAGDVHVSIIKSRIGQMSNRNMG 187
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 209 SNMOSNAYLNGQSLSPFRVTTTDDGETRVFODIVPVSWTFEGQTF 249
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 188 NMOSNAYLNGQSLSPFRVTTSDQITVSNMKNANAGMSFGQTF 228

RESULT 13
US-08-440-517A-6
; Sequence 6, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GULLITTAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
US-08-440-517A-6

Query Match 61.4%; Score 861; DB 1; Length 226;

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; APPLICANT: Cosgrove, Daniel J
; TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
; FILE REFERENCE: 11940E183
; CURRENT APPLICATION NUMBER: US/09/071,252C
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: 60/045,445
; EARLIER FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-09-071-252-22

Query Match      63.2%; Score 886.5; DB 2; Length 250;
Best Local Similarity 65.4%; Pred. No. 3.3e-81;
Matches 161; Conservative 30; Mismatches 50; Indels 5; Gaps 4;

QY 10 SLIGLCCTTTTAAFPSPGHTNAHATFYGGSDASGTMGACGYGNLYATGYGTRTALST 69
DB 10 SLFLPFFVFTPA-DYGGQSGHATFYGGSDASGTMGACGYGNLYSQGTGNTVALST 68
QY 70 ALFNDGASCGQCYKIICDYKSDSRWCIGRSVVTATNFCPPFPALPNNNGWCNPLK 129
DB 69 ALFNNGLSCACCEMTC--TNDPKCLPG-TIRVTATNFCPPFPALPNNNGWCNPLKH 125
QY 130 FDMAQPAWKIGYIRGIVPVLFQRYPCCKGGRSVNGRDYFELVLSNVGAGSIO 189
DB 126 FDMAEAPAIQIAQYRAIVPVSRVPCMKKGVRFTINGHSYFNLVLTNVGAGDVHS 185
QY 190 VFKSGKTGMANSRWGSMQSNAYLNGQSLSPRTTDDGTRVQDIPVSWTQGT 249
DB 186 VSTKSGRTQWMSRWGMQSNAYLNGQSLSPVLTSLDGRITLAVNLPVSMQFGQY 245
QY 250 SSPVQF 255
DB 246 EGP-QF 250

RESULT 9
US-08-440-517A-2
; Sequence 2, Application US/08440517A
; Patent No. 5958082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228
; TYPE: AMINO ACID
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; TOPOLOGY: UNKNOWN
US-08-440-517A-2

Query Match      63.0%; Score 884.5; DB 1; Length 228;
Best Local Similarity 67.7%; Pred. No. 4.6e-81;
Matches 151; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 28 GWTNAHATFYGGSDASGTMGACGYGNLYATGYGTRTALSTALPNDGASCGQCYKICD 87
DB 4 GWTNAHATFYGGSDASGTMGACGYGNLYSQGTGNTALSTALPNNGLSCGACFEIR 62
QY 88 YKSDSRWCIGRSVVTATNFCPPFPALPNNNGWCNPLKFDMAQPAWKIGYIRG 147
DB 63 -QNDGKMCCLPG-SIVVTATNFCPPNNAALPNNAGWCNPPQHFDSIQPVFORIAQYRAGI 120
QY 148 VPVLFQRYPCCKGGRSVNGRDYFELVLSNVGAGSIOGVFTKSGKTGMANSRW 207
DB 121 VPVAYRVPQVRRGIRFTINGHSYFNLVLTNVGAGDVHSAMVYGSRTGMQMSRW 180
QY 208 SNWQSNAYLNGQSLSPRTTDDGTRVQDIPVSWTQGTFS 250
DB 181 QMWQSNAYLNGQSLSPKVTTSDDGRTIVSNNAAGMSFQGTFT 223

RESULT 10
US-09-092-160-2
; Sequence 2, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guiltinan, Mark J
; APPLICANT: Scherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C14US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: rice expansin
; NAME/KEY: UNSURE
; LOCATION: 211
; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-2

Query Match      63.0%; Score 884.5; DB 2; Length 228;
Best Local Similarity 67.7%; Pred. No. 4.6e-81;
Matches 151; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 28 GWTNAHATFYGGSDASGTMGACGYGNLYATGYGTRTALSTALPNDGASCGQCYKICD 87
DB 4 GWTNAHATFYGGSDASGTMGACGYGNLYSQGTGNTALSTALPNNGLSCGACFEIR 62
QY 88 YKSDSRWCIGRSVVTATNFCPPFPALPNNNGWCNPLKFDMAQPAWKIGYIRG 147
DB 63 -QNDGKMCCLPG-SIVVTATNFCPPNNAALPNNAGWCNPPQHFDSIQPVFORIAQYRAGI 120
QY 148 VPVLFQRYPCCKGGRSVNGRDYFELVLSNVGAGSIOGVFTKSGKTGMANSRW 207
DB 121 VPVAYRVPQVRRGIRFTINGHSYFNLVLTNVGAGDVHSAMVYGSRTGMQMSRW 180
```

```

? GENERAL INFORMATION:
? APPLICANT:
? TITLE OF INVENTION: MICROBIAL SMOLLENTIN PROTEIN, DNA SEQUENCES
? TITLE OF INVENTION: ENCODING SUCH SMOLLENTINS AND METHOD OF PRODUCING SUCH
? TITLE OF INVENTION: SMOLLENTINS
? NUMBER OF SEQUENCES: 31
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/112,498A
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 98/14226
? FILING DATE:
? APPLICATION NUMBER: US 08/893,766
? FILING DATE: 11-JUL--1997
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 237 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
?
US-09-112-498A-7

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	Query Match	63.5%	Score 890.5	DB 2	length 237	
	Best Local Similarity	66.5%	Pred. No. 1.2e-81			
	Matches 151,	Conservative 35,	Mismatches 38,	Indels 3,	Gaps 2,	
<hr/>						
QY	24	PSPSGWTNAHAATFYGGSDASGTMGACGYGNLYATGYCTRTAALSTALENDGASCOCGYK	83			
	:	: :	:	:	:	:
Db	9	YAGGGMVAHAATFYGGDGASGTMGACCGYNLISGXYGTNTAAALSTALENNGLSCGCFE	68			
<hr/>						
QY	84	IICDYSRRCIGRASVTYTATNCPENPALPNNNGCMCPPLKHFDMAAPABEKI G I Y	143			
	:	: : :	:	:	:	:
Db	69	IRC--QNDGRKCLPG-SIVTAINFCPPNNALLPNNAGMCMFPQGHFPLSDPVVRILOX	125			
<hr/>						
QY	144	RGGIVPYLPFORVPCKRHGVRFVSNGRDYFEILVLSINVGAGSIOISVPIKSKKTGMAMS	203			
	:	: : : : :	:	:	:	:
Db	126	RAGIVPAVYRRVPCVRRGIRIFPTINGHSYFNVLVLTITNVGADVDHSAWVKSRFTQMMS	185			
<hr/>						
QY	204	RNKSSNMNSAYLNQGSLSPRYTTIDESTRYEQDLVPVSWTRGQTFS	250			
	:	: : : : :	:	:	:	:
	186	RNWQQNQMSNLINGQSLSFRVYTTISDDGITVISNNVANAGMBFGQFT	232			

RESULT 6
US-09-071-252-37
Sequence 37, Application US/09071252C
Patent No. 6682738
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
FILE REFERENCE: 119408183
CURRENT APPLICATION NUMBER: US/09/071,252C
CURRENT FILING DATE: 1998-05-01
EARLIER APPLICATION NUMBER: 60/045,445
EARLIER FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 254
TYPE: PRT
ORGANISM: Arabidopsis
US-09-071-252-37

Query Match	63.5%	Score 890.5;	DB 2;	Length 254;
Best Local Similarity	66.5%;	Pred. No. 1.3e-81;		
Matches 151;	Conservative 35;	Mismatches 36;	Indels 3;	Gaps 2;
OY	24	FSPSGMTAAHATFYGGSDASGTMGACGYNLYATGYGTRTAAALSTALFNDGASCGGQYK	83	

Db 26 YAGGGVNNAAHAFYGGGDASGTMGGAACGYGNLYSQGYGTWTAALSTALFNNNGSCGACFE 85
 Qy 84 IICDYKSDSRMCIKKRSYTTATATNFCPNFALPNNNGMCNPLPKHEDMAQPAHEKIGY 143
 Db 86 IRC--QNDCKWCLPG-SIVWTATNFCPPNNNALPNNAGGMCNPPQHFDLSQPFVORIAQY 142
 Qy 144 RGSIVPYLEFORVPCKKHGGVRSVUNGDDYFELVLISNVGAGSISQYFIKSGTKTGMMAMS 203
 Db 143 RAGIVPVAIRVPVCVRGGIRFTINGHSYFNLVLTIVNGAGDVHSAHVGRSGRTGQAMS 202
 Qy 204 RNMGSNMGSNAYLINGQSLSFRVTTTGGSTRVFDIVPVSMTFGQTS 250
 Db 203 RNMGSNMGSNAYLINGQSLSFKTTTSDGQTIYSNNVAANAGMSFGQTF 249

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1      RESULT 7
2      US-09-112-498A-5
3      ; Sequence 5, Application US/09112498A
4      ; Patent No. 6458928
5      ; GENERAL INFORMATION:
6      ; APPLICANT:
7      ; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
8      ; TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
9      ; TITLE OF INVENTION: SWOLLENINS
10     ; NUMBER OF SEQUENCES: 31
11     ; COMPUTER READABLE FORM:
12     ; MEDIUM TYPE: Floppy disk
13     ; COMPUTER: IBM PC compatible
14     ; OPERATING SYSTEM: PC-DOS/MS-DOS
15     ; SOFTWARE: Patentn Release #1.0, Version #1.25 (EPO)
16     ; CURRENT APPLICATION DATA:
17     ; APPLICATION NUMBER: US/09/112,498A
18     ; FILING DATE:
19     ; PRIOR APPLICATION DATA:
20     ; APPLICATION NUMBER: US 98/14226
21     ; FILING DATE:
22     ; APPLICATION NUMBER: US 08/893,766
23     ; FILING DATE: 11-JUL-1997
24     ; INFORMATION FOR SEQ ID NO: 5:
25     ; SEQUENCE CHARACTERISTICS:
26     ; LENGTH: 227 amino acids
27     ; TYPE: amino acid
28     ; TOPOLOGY: unknown
29     ; MOLECULE TYPE: protein
30     ; US-09-112-498A-5

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	Query Match	63.4%	Score 889	DB 2	length 221
	Best Local Similarity	68.4%	Pred. No. 1.66-81		
	Matches	156	Conservative 28	Mismatches 40	Indels 4
				Gaps	3
QY	28	GWTAAATFTYGGASGTMGACGCGNLXAGYCTRTAAALSTALFNDGASGCGCYKII	CD	87	
DB	4	GMGGHATFTYGGGASGTMGACGCGNLXSGYGTNTVALSTALFNNGLSGCAAFEMTC	-	62	
QY	88	YKSDSRMCIKGRSVTVYATNFCPPNFALPNNNGCMCPNLKGFMDAPAMEKIGIYRGI		147	
DB	63	-TNPKNCLPG-TIRVTAINTFCPPNFALPNNNGCMCPNLPHFMDABEAFIQIDQYRGI		120	
QY	148	VPVLFQRYVPCKKGGVAFPSVNGRDYFELVILISNVGAGSIQSVFIKSGSKTGMAMSRNG		207	
DB	121	VPVAFRRVPCKMKGGVAFPTINGHSYFNLVLTITNGAGADIVASVIKGSRTQMGMSRWG		180	
QY	208	SNMGSMAYLNGQSLSFRVTTTDDSTRVPQDILVPISWTFQCGFFSSFPVQ		255	
DB	181	QNMGSNNYLNQGLSFOVTLSDGNTLTAYNLVPSNMGFGQGYEGP-QP		227	

RESULT 8
US-09-071-252-22
; Sequence 22, Application US/09071252C
; Patent No. 6682738
; GENERAL INFORMATION:


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; TITLE OF INVENTION: SWOLLENINIS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-112-498a-6

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Query Match      78.2%; Score 1097.5; DB 2; Length 234;
Best Local Similarity 82.8%; Pred. No. 1.6e-102;
Matches 193; Conservative 21; Mismatches 18; Indels 1; Gaps 1;

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```

QY 24 FSDSGWTAHATYGGSDASGTWGAACGYGNLYATGYGRTALSTALFNDGASCGQCYK 83
   |||
DB 1 FTASGWAHATYGGSDASGTWGAACGYGNLYATGYGRTALSTALFNDGASCGQCYK 60
QY 84 IICDYSDSRWCKIGSVYTTATNFCBPNNALPNNNGWGNPPLKHPDAPAMKIGTY 143
   |||
DB 61 IICDYTDPRWCKIGSVYTTATNFCBPNNALPNNNGWGNPPLKHPDAPAMKIGTY 120
QY 144 RGGIVFVLFQVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIOGVFIKSK-TGMMAM 202
   |||
DB 121 RGGIIVLVQVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIOGVFIKSK-SNMWTPM 180
QY 203 SRWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTFSSVQF 255
   |||
DB 181 SRWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTFSSVQF 233

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RESULT 3
US-09-071-252-36
; Sequence 36, Application US/09071252C
; Patent No. 6682738
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
; FILE REFERENCE: 11940E183
; CURRENT APPLICATION NUMBER: US/09/071,252C
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: 60/045,445
; EARLIER FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-09-071-252-36

```

```

Query Match      74.1%; Score 1039; DB 2; Length 261;
Best Local Similarity 73.2%; Pred. No. 1.5e-96;
Matches 180; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

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QY 10 SLIGLCCFTTTTAFSPSGWTAHATYGGSDASGTWGAACGYGNLYATGYGRTALST 69
   |||
DB 15 ALIATCILMEASFTASGWNKAFAFYGGSDASGTWGAACGYGDLVSTGYGRTALST 74

```

```

QY 70 ALFNDGASCGQCYKIIICDYSDSRWCKIGRSVYTTATNFCBPNNALPNNNGWGNPPLKH 129
   |||
DB 75 VLFNDGASCGQCYRIMCQADRRFCISGTVIATNLCPPNYALPNDAGWGNPPLKH 134
QY 130 FPMAGPAMEKIGTYGGIVPVLPFQVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIO 189
   |||
DB 135 FPMASPAWKIGTYGGIVPVLPFQVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIO 194
QY 190 VFIKSKTGMWMSNRWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTF 249
   |||
DB 195 VFIKSKTGMWMSNRWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTF 254
QY 250 SSPVQF 255
   |||
DB 255 STSQGF 260

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```

RESULT 4
US-09-112-498a-3
; Sequence 3, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
; FILE REFERENCE: ENCODING SUCH SWOLLENINIS AND METHOD OF PRODUCING SUCH
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-112-498a-3

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Query Match      65.8%; Score 923; DB 2; Length 223;
Best Local Similarity 72.5%; Pred. No. 5.9e-85;
Matches 161; Conservative 27; Mismatches 30; Indels 4; Gaps 3;

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```

QY 28 GWTNAHATYGGSDASGTWGAACGYGNLYATGYGRTALSTALFNDGASCGQCYKICD 87
   |||
DB 2 GWSAHATYGGSDASGTWGAACGYGNLYATGYGRTALSTALFNDGASCGQCYKICD 61
QY 88 YKSDSRWCKIGRSVYTTATNFCBPNNALPNNNGWGNPPLKHPDAPAMKIGTYRGT 147
   |||
DB 62 --NDPFWCLPG-SIYTTATNFCBPNNALPNNNGWGNPPLKHPDAPAMKIGTYRGT 118
QY 148 VPLVFPQVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIOGVFIKSKTGMWMSNRNG 207
   |||
DB 119 VPLVARYVPCCKKHGVRFSVNGRDYFELVLIISNVGAGSIOGVFIKSKTGMWMSNRNG 178
QY 208 SNWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTF 249
   |||
DB 179 QNWGSNWSNAYLNGQSLSFRTYTTDGETRFQDIYVPSWTFGQTF 219

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```

RESULT 5
US-09-112-498a-7
; Sequence 7, Application US/09112498A
; Patent No. 6458928

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2006, 12:32:04 ; Search time 46 Seconds

(without alignments)
458.311 Million cell updates/sec

Title: US-10-660-499A-2

Perfect score: 1403

Sequence: 1 MKKIMVLGSLGLCCFTT.....QDIVPVSMTFGQTSSPVQF 255

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/6.COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H.COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCUS.COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RR.COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103.5	78.7	258	2	US-09-071-252-23
2	1097.5	78.2	224	2	US-09-112-498A-6
3	1039	74.1	261	2	US-09-071-252-36
4	923	65.8	223	2	US-09-112-498A-3
5	890.5	63.5	237	2	US-09-112-498A-7
6	890.5	63.5	254	2	US-09-071-252-37
7	889	63.4	227	2	US-09-112-498A-5
8	886.5	63.2	250	2	US-09-071-252-22
9	884.5	63.0	228	1	US-08-440-517A-2
10	884.5	63.0	227	2	US-09-092-160-2
11	879	62.7	227	2	US-09-092-160-7
12	870.5	62.0	233	2	US-09-112-498A-11
13	861	61.4	226	1	US-08-440-517A-6
14	861	61.4	226	2	US-09-092-160-6
15	855	60.9	232	2	US-09-112-498A-8
16	826.5	58.9	233	2	US-09-112-498A-13
17	817.5	58.3	233	2	US-09-112-498A-12
18	816.5	58.2	241	2	US-09-112-498A-10
19	803	57.2	233	2	US-09-112-498A-9
20	794.5	56.6	225	1	US-08-440-517A-5
21	794.5	56.6	225	2	US-09-092-160-5
22	773	55.1	222	1	US-08-440-517A-3
23	773	55.1	222	2	US-09-092-160-3
24	768.5	54.8	227	1	US-09-362-642-2
25	767	54.7	227	1	US-08-440-517A-4
26	767	54.7	227	2	US-09-092-160-4
27	763.5	54.4	225	1	US-08-845-539-2

28	678.5	48.4	179	1	US-08-845-539-6	Sequence 6, Appl1
29	678.5	48.4	179	2	US-09-362-642-6	Sequence 6, Appl1
30	618.5	44.1	167	1	US-08-845-539-4	Sequence 4, Appl1
31	618.5	44.1	167	2	US-09-362-642-4	Sequence 21, Appl1
32	302.5	21.6	258	2	US-09-071-252-21	Sequence 9, Appl1
33	302.5	21.6	259	2	US-09-071-252-9	Sequence 17, Appl1
34	291.5	20.8	273	2	US-09-071-252-17	Sequence 12, Appl1
35	262.5	18.7	260	2	US-09-071-252-12	Sequence 10, Appl1
36	257	18.3	261	2	US-09-071-252-10	Sequence 11, Appl1
37	257	18.3	295	2	US-09-071-252-11	Sequence 2, Appl1
38	243	17.3	261	1	US-07-971-096-2	Sequence 18, Appl1
39	243	17.3	261	1	US-08-175-096-2	Sequence 19, Appl1
40	242.5	17.3	269	2	US-09-071-252-18	Sequence 13, Appl1
41	240.5	17.1	263	2	US-09-071-252-19	Sequence 21, Appl1
42	240.5	17.1	283	2	US-09-071-252-13	Sequence 4, Appl1
43	234.5	16.7	246	2	US-08-441-507-21	Sequence 21, Appl1
44	234.5	16.7	246	2	US-07-969-875A-21	Sequence 4, Appl1
45	232.5	16.6	263	1	US-07-971-096-4	

ALIGNMENTS

```
RESULT 1
US-09-071-252-23
Sequence 23, Application US/09071252C
Patent No. 6682738
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
FILE REFERENCES: 11940E183
CURRENT APPLICATION NUMBER: US/09/071,252C
EARLIER FILING DATE: 1998-05-01
EARLIER APPLICATION NUMBER: 60/045,445
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 258
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-071-252-23

Query Match      78.7%; Score 1103.5; DB 2; Length 258;
Best Local Similarity 81.2%; Pred. No. 4,6e-103;
Matches 195; Conservative 22; Mismatches 22; Indels 1; Gaps 1;

QY      17 FTTTTFAPBSGWTNMAHATFYGSDASGTMGACGYGNLYATGYGTRTALSTALPRDGA 76
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      18 FFLFVNAFPTASGMAPAHATFYGESDASGTMGACGYGNLYQTGYGTRTALSTALPRDGA 77

QY      77 SCGQCKRTICDYSDBRWCKKGSVYVTAATNFCPPPALPNNNGWCNPLKHFMAOPA 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      78 SCGQCKRTICDYSDBRWCKKGSVYVTAATNFCPPPALPNNNGWCNPLKHFMAOPA 137

QY      137 MERKIGYRGIVVLFQRYPCCKHGVRSVNGRDYFELVLSNMGAGSIOGFTKSK 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      138 MOKIGYRGIVVLFQRYPCCKHGVRSVNGRDYFELVLTNMGAGADIKSVTSKSK 197

QY      197 TGMAMSRNWSNMGOSNAYLNGQISFRVTTTDSGTRVFDIVPVSMTFGQTSSPVQF 255
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      198 SSMWTMRSRWGANMOSNAYLNGQISFRVTTTDSGTRVFDIVPVSMTFGQTSSPVQF 257

RESULT 2
US-09-112-498A-6
Sequence 6, Application US/09112498A
Patent No. 6458928
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
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; SEQ ID NO 6
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: anti-human CD3 reshaped scfv amino acid sequence of heavy chain
; US-10-478-345-6
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Query Match          5.6%; Score 78; DB 6; Length 357;
Best Local Similarity 39.1%; Pred. No. 3.1;
Matches 27; Conservative 2; Mismatches 34; Indels 6; Gaps 3;
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```
QY      13  GLCFTITTYAPSPSGMTNNAHATFYGSDASGTMGACGYGNLYATGYGTRTALSTALF 72
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      244  GACC---TGAGAACTGTGAGATCTGACGAC-TCGCCCCGTGTACTACTGTGTAGATACT 298
QY      73  NDGASCGQC 81
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DB      299  ACGA-CGAC 306
```

Search completed: January 10, 2006, 12:41:12
Job time : 9 secs

Db 1324 GKVGSVYANARAIQRAQSIIGRYKSSYTEQWVRVAKRESNFGSDAVNNMDINAKRG 1383
 QY 226 TTTDGETRVFODIVP 240
 Db 1384 TPKSG--MFMQIEP 1395

RESULT 12

US-11-052-554A-285
 ; Sequence 285, Application US/11052554A
 ; Publication No. US2005028866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sachdeva, et al.
 ; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
 ; FILE REFERENCE: 30853/40359A
 ; CURRENT APPLICATION NUMBER: US/11/052,554A
 ; PRIOR FILING DATE: 2005-02-07
 ; PRIOR APPLICATION NUMBER: US 60/589,227
 ; PRIOR FILING DATE: 2004-07-20
 ; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
 ; PRIOR FILING DATE: 2004-02-06
 ; NUMBER OF SEQ ID NOS: 763
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 285
 ; LENGTH: 547
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli 0157:H7
 ; US-11-052-554A-285

Query Match 5.7%; Score 80; DB 7; Length 547;
 Best Local Similarity 22.8%; Pred. No. 3.2; 97; Indels 80; Gaps 11;
 Matches 59; Conservative 23; Mismatches

QY 19 ITTYAFSPSGWTNAHATFYGSDASGTMGACGYGMLY-----ATGY-----GTRTA 65
 |||||
 Db 65 ITGDTADPSG-----NLGVMTPAAGTNGINMGDVTVNVADAGYAKGIIIGKNS 118
 QY 66 ALSTALFND--GASCGQCKIICDY-----KSDSRMCIKRSYTVTRATNCPFN 112
 |||||
 Db 119 LTRNRLTVVVGQTSAGINLIGDYTHADLGTGSKTSDNDGIIISHSTLTATOPTIEN 178
 QY 113 PALPNNNGWMCNPLKHPDMAQPAWEK---IGYRGIVPVLFQVPCCKHGVAFSVN 168
 |||||
 Db 179 ---SNIGLTINDYGSVDIGSSKIKTDGSTVIYIGL-----N 215
 QY 169 GRDYFELVLISNAGASIQSVFIKSGKTGMAMSRNWSNMQSNAYLNGQSLSPRVTTT 228
 |||||
 Db 216 G-----NNANGAARFATDLTIDVGYSAM-----GINVQKNSVVD-----LGT 254
 QY 229 DGETRVFODIVPVSWTFQG 247
 |||||
 Db 255 NSSIKTSGDNAHGLMSFGQ 273

RESULT 13

US-11-080-991-104
 ; Sequence 104, Application US/11080991
 ; Publication No. US20050266437A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velby, Peter Ole
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
 ; FILE REFERENCE: MRI-039
 ; CURRENT APPLICATION NUMBER: US/11/080,991
 ; PRIOR FILING DATE: 2005-03-11
 ; PRIOR APPLICATION NUMBER: US/10/116,847
 ; PRIOR FILING DATE: 2002-06-21
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 104
 ; LENGTH: 522

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-080-991-104

Query Match 5.6%; Score 79; DB 7; Length 522;
 Best Local Similarity 31.4%; Pred. No. 3.8; 32; Indels 10; Gaps 2;
 Matches 22; Conservative 6; Mismatches

QY 4 IMLVGSILIGLCFTTITTYAFSPSGWTNAHATF-----YGSDDASGTMGACGYGN 54
 ::|||
 Db 64 VIRIISMLIIVWCIAIFACVASTLAMDRGYISLGGSVGYGGG--GRGSYGSYGYGY 122
 QY 55 LYATSYGTRT 64
 |||||
 Db 123 GYGYGYGYT 132

RESULT 14

US-10-515-868-8
 ; Sequence 8, Application US/10515868
 ; Publication No. US20050282729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hamilton, David W
 ; APPLICANT: Robert, Kenneth P
 ; APPLICANT: Ensrud, Kathy M
 ; TITLE OF INVENTION: CRISP POLYPEPTIDES AS CONTRACEPTIVES AND INHIBITORS OF SPERM
 ; FILE REFERENCE: 110,01860101
 ; CURRENT APPLICATION NUMBER: US/10/515,868
 ; PRIOR FILING DATE: 2004-11-24
 ; PRIOR APPLICATION NUMBER: 60/383,628
 ; PRIOR FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: PCT/US03/16669
 ; PRIOR FILING DATE: 2003-05-28
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 1886
 ; TYPE: PRT
 ; ORGANISM: HOMOSAPIEN
 ; US-10-515-868-8

Query Match 5.6%; Score 78.5; DB 6; Length 1886;
 Best Local Similarity 29.1%; Pred. No. 18;
 Matches 30; Conservative 5; Mismatches 53; Indels 15; Gaps 3;

QY 13 GLCCFTTITTYAFSPSGWTNAHATFYGSDASGTMGACGYGMLYATGYGTRTALSTALF 72
 |||||
 Db 1098 GTCCCTCAACA-----GTAACTGGGCTAAATAAGTTC---TTATGTGTTCAACTGCC 1148
 QY 73 NGASGCGCYKTIICDYKSDSRMCIK-----GRSVTVTATNFC 109
 |||||
 Db 1149 ACCCCGCTTCCCATATTTCACACTCTGATTAATCTTC 1191

RESULT 15

US-10-478-345-6
 ; Sequence 6, Application US/10478345
 ; Publication No. US2005025515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Institute of Genetics and Devel. Biol, CAS
 ; APPLICANT: Dongguan Haofa Biotechnology Developmental Co., Ltd.
 ; TITLE OF INVENTION: Anti Human Ovarian Cancer- Anti CD3 Bispecific Antibody
 ; FILE REFERENCE: US3-2-11393-US01
 ; CURRENT APPLICATION NUMBER: US/10/478,345
 ; PRIOR FILING DATE: 2003-11-21
 ; PRIOR APPLICATION NUMBER: CN 01118247.4
 ; PRIOR FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: PCT/CN02/00347
 ; PRIOR FILING DATE: 2002-05-23
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (221)..(227)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-670-009-4

Query Match 54.7%; Score 767; DB 6; Length 227;
Best Local Similarity 63.6%; Pred. No. 3, 1e-64;
Matches 136; Conservative 28; Mismatches 48; Indels 2; Gaps 2;

QY 31 NNAATFYGGSDASGTWGAAGYGNLYATGYGTRTALSTALFNDGASCGQCYKIICDYKS 90
DB 7 SAFAFYGGKSDSCMTGAGAGYGNLYATGYGTRTALSTALFNDGAMGACYTITCD-7S 65
QY 91 DSRWCIK-GRSVTTATNFPCPNFALPNNNGWCNPLKHPMAOPAMEKIGIRGGLV 149
DB 66 QTKWCKPGGNSITITATNLCXPNMALPSNSGGCNPLXHPMSOPAMENIAYVQAGIVP 125
QY 150 VLPORVPCCKHGVRSVNGRDPYFELVLIISNVGAGSISQSVFIKSGSKTGMMAMSRMGSN 209
DB 126 VVYKRPVCKRSGIRFALISGHDIFELVLTYNVGGSGVAVQMSIKSNTGMAMSRMGAN 185
QY 210 WQSNATLNGQSLSPRYTTTDDGTRVFODIVPVSW 243
DB 186 WQSNATLNGQSLSTFVQLDGRKVTAMNAPXNW 219

RESULT 7
US-10-670-009-3
Sequence 3, Application US/10670009
Publication No. US20050272041A1
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J.
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark
APPLICANT: Shcherban, Tatyana
APPLICANT: Jun, Shi
TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
FILE REFERENCE: P04660508
CURRENT APPLICATION NUMBER: US/10/670,009
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 09/896,301
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 09/429,675
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 08/834,327
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 08/444,515
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: US 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: US 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)..(15)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)..(20)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (58)..(58)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-670-009-3

Query Match 54.0%; Score 758; DB 6; Length 222;
Best Local Similarity 59.5%; Pred. No. 2, 1e-63;
Matches 132; Conservative 36; Mismatches 44; Indels 10; Gaps 2;

QY 29 WTNAAATFYGGSDASGTWGAAGYGNLYATGYGTRTALSTALFNDGASCGQCYKIICDY 88
DB 5 WTNAAATFYXXGDXATXWGAAGYGNLYSGYGLSTALSTALFNDGASCGAXELMC-- 62
QY 89 KDSRWCIKGRSVTTATNFPCPNFALPNNNGWCNPLKHPMAOPAMEKIGIRGGLV 148
DB 63 VMDPQWCIAGRSIVVTATNFCPP-----GACDPPIHHPDLSPPIYEXIALYKSGII 114
QY 149 PVLPRVPCCKHGVRSVNGRDPYFELVLIISNVGAGSISQSVFIKSGSKTGMMAMSRMGSN 208
DB 115 PVMYRRVCKRSGGIRFTINGSHFNLTALVTYNVGGAGDVHVSMSKSRKTMQJMSRMQ 174
QY 209 WQSNATLNGQSLSPRYTTTDDGTRVFODIVPVSWTFQGTFS 250
DB 175 WQSNATLNGQSLSTFVTTSDRSVSVFVAPPTWSFGQTYT 216

RESULT 8
US-11-170-653-16
Sequence 16, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 213
TYPE: PRT
ORGANISM: Bacillus subtilis
US-11-170-653-16

Query Match 6.3%; Score 88; DB 7; Length 213;
Best Local Similarity 18.9%; Pred. No. 0.2;
Matches 46; Conservative 32; Mismatches 87; Indels 78; Gaps 13;

QY 10 SLIGLCCPTITTYAPSPSCWTAAHATFYGGSDASGTWGAAGYGNLYATGYGTRTALST 69
DB 15 ALMSISLFSATASASTDWQN-----WTGGGIVAVNDSGGNTSVNMSN---TGN 63
QY 70 ALFNDGASCGQCYKIICDYKSDSRWCIKGRSVTTATNFPCPNFALPNNNG-----GWNC 124
DB 64 FVVGKWTITGSPRIT-NTNA-GWA-----PENGGLTLYGWTR 101
QY 125 PVLKHPMAOP--AMEKIGIRGGLVPLPVRVPCCKHGG-----VAP---SVNG--- 169
DB 102 SPLIEYVVDSWGYRPFYTGTV-----KSDGTYDIYTTTNNAPSIDGDT 151
QY 170 --RDYFELVLIISNVGAGSISQSVFIKSGSKTGMMAMSRMGSNWQSNATLNGQSLSPRYTT 227
DB 152 TTFQWMS--VROSKRPTGSNATITPSNHYNAKSHQMTGSKW-----ATQWA 198
QY 228 TDG 230

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; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: US 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-670-009-6
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Query Match          60.7%; Score 852; DB 6; Length 226;
Best Local Similarity 66.8%; Pred. No. 4.2e-72;
Matches 149; Conservative 29; Mismatches 41; Indels 4; Gaps 3;
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QY      27 SGMTHAATFYGGSDASGTMGACGYNLYATGYGTRTALSTALPNDGASCGQCYKIC 86
      3 SSMQSHATFYGGSDASGTMGACGYNLYSTGY-TNTALSTVLPNDGACGSCYELNC 61
QY      87 DYKSDSRMCIKGRSVTVTATNFCPPNPALPNNNGWCNPLKHPDMAQPAHEKIGIYRG 146
      62 D--NDQWCLPG-SVTVTATNLCPPYVALPNDGWCNPPRPHDMAEPALQIGYRRAG 118
QY      147 IVPVLPORVPCKKGGRVSVNGRDYFELVLTISNVGAGSISGVFIKSGTKGMAMSRM 206
      119 IVPVSTRVPCKKGGIRFTINGHSTFNLVLTNVAGPGDVQSVISKSGSTGMQPSRM 178
QY      207 GSNMGSNAYLNGSLSFRVTTTIDGTRVPDIIVPVSWTFGQTF 249
      179 GQNMGSNTYLDGQSLSFQVAVSDGRTVTSNNVVPADMQFGQTF 221
DB
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```

RESULT 5
US-10-670-009-5
; Sequence 5, Application US/10670009
; Publication No. US20050272041A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J.
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guillemin, Mark
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Jun, Shi
; TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
; FILE REFERENCE: P04666US08
; CURRENT APPLICATION NUMBER: US/10/670,009
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 09/896,301
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/429,675
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 08/834,327
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 08/444,515
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: US 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: US 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-670-009-5
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Query Match          57.0%; Score 799.5; DB 6; Length 225;
Best Local Similarity 64.6%; Pred. No. 3e-67;
Matches 144; Conservative 28; Mismatches 44; Indels 7; Gaps 4;
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QY      28 GMTNAHATFYGGSDASGTMGACGYNLYATGYGTRTALSTALPNDGASCGQCYKICD 87
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```

DB      4 GMRGHATFYGGSDASGTMGACGYNLHSGYGLTALSTALPNSGQKCACFPLTJB 63
QY      88 YKSDSRMCIKGRSVTVTATNFCPPNPALPNNNGWCNPLKHPDMAQPAHEKIGIYRG 147
      64 --DDPEWCIPGS--IIVRTNLA--NPAANDNGWCNPLKHPDLAEPALQIAQYRAGI 117
QY      148 VPVLPORVPCKKGGRVSVNGRDYFELVLTISNVGAGSISGVFIKSGTKG--MMAMSRM 206
      118 VPVAFPRVPCKKGGRIRFTINGHSTFNLVLTNVGAGDGRVLSKSGTKDQMPSRM 177
QY      207 GSNMGSNAYLNGSLSFRVTTTIDGTRVPDIIVPVSWTFGQTF 249
      178 GQNMGSNTYLRQSLSFQVAVSDGRTVSYDVVPHDMQFGQTF 220
DB
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RESULT 6
US-10-670-009-4
; Sequence 4, Application US/10670009
; Publication No. US20050272041A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J.
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guillemin, Mark
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Jun, Shi
; TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
; FILE REFERENCE: P04666US08
; CURRENT APPLICATION NUMBER: US/10/670,009
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 09/896,301
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/429,675
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 08/834,327
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 08/444,515
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: US 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: US 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (86)..(86)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (104)..(104)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (214)..(214)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; NAME/KEY: misc feature
; LOCATION: (217)..(217)
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OM protein - protein search, using SW model

Run on: January 10, 2006, 12:35:09 ; Search time 9 Seconds
(without alignments)
240.653 Million cell updates/sec

Title: US-10-660-499a-2

Perfect score: 1403
Sequence: 1 MKKIMLVLSLIGLCFFITT.....QDIVPVSWTGGTSSPVQF 255

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
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8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	100.0	255	6	US-10-660-499a-2
2	884.5	63.0	228	6	US-10-670-009-2
3	879	62.7	227	6	US-10-670-009-7
4	852	60.7	226	6	US-10-670-009-6
5	799.5	57.0	225	6	US-10-670-009-5
6	767	54.7	227	6	US-10-670-009-4
7	758	54.0	222	6	US-10-670-009-3
8	88	6.3	213	7	US-11-170-653-16
9	87	6.2	213	7	US-11-170-653-17
10	82.5	5.9	2399	7	US-11-052-554A-92
11	80.5	5.7	1572	6	US-10-793-626-2906
12	80	5.7	547	7	US-11-052-554A-285
13	79	5.6	522	7	US-11-080-991-104
14	78.5	5.6	1886	6	US-10-515-868-8
15	78	5.6	357	6	US-10-478-345-6
16	78	5.6	955	7	US-11-052-554A-179
17	77	5.5	240	7	US-11-170-653-38
18	76.5	5.5	1574	6	US-10-055-877-211
19	76	5.4	339	6	US-10-878-556A-18
20	76	5.4	339	6	US-10-995-561-681
21	76	5.4	339	6	US-10-995-561-682
22	76	5.4	339	6	US-10-995-561-684
23	76	5.4	339	6	US-10-995-561-685
24	76	5.4	339	6	US-10-995-561-686
25	76	5.4	339	6	US-10-995-561-687

26	76	5.4	339	7	US-11-186-284-43	Sequence 43, Appl
27	76	5.4	344	6	US-10-821-234-923	Sequence 923, App
28	75.5	5.4	967	6	US-10-995-561-979	Sequence 979, App
29	75.5	5.4	967	6	US-10-995-561-980	Sequence 980, App
30	75.5	5.4	999	6	US-10-821-234-1251	Sequence 1251, App
31	74	5.3	1018	7	US-11-067-121-17	Sequence 17, Appl
32	74	5.3	1218	7	US-11-078-735-20	Sequence 20, Appl
33	74	5.3	1238	7	US-11-078-735-21	Sequence 21, Appl
34	74	5.3	1403	6	US-10-055-877-52	Sequence 52, Appl
35	74	5.3	2105	7	US-11-052-554A-173	Sequence 173, App
36	74	5.3	3194	7	US-11-052-554A-90	Sequence 90, Appl
37	74	5.3	3714	6	US-10-995-561-1015	Sequence 1015, App
38	73.5	5.2	544	6	US-10-980-388-40	Sequence 40, Appl
39	73.5	5.2	1398	6	US-10-055-877-46	Sequence 46, Appl
40	73.5	5.2	1404	6	US-10-055-877-44	Sequence 44, Appl
41	73.5	5.2	1577	6	US-10-055-877-54	Sequence 54, Appl
42	73	5.2	346	7	US-11-016-564-18	Sequence 18, Appl
43	73	5.2	3011	6	US-10-985-205-3	Sequence 3, Appl
44	72.5	5.2	311	6	US-10-793-626-3080	Sequence 3080, App
45	72.5	5.2	420	6	US-10-131-826A-290	Sequence 290, App

ALIGNMENTS

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RESULT 1
US-10-660-499a-2
; Sequence 2, Application US/1060499a
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG-KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-660-499a-2

Query Match      100.0%; Score 1403; DB 6; Length 255;
Best Local Similarity 100.0%; Pred. No. 4, 9e-123; Indels 0; Gaps 0;
Matches 255; Conservative 0; Mismatches 0;

QY      1  MKKIMLVLSLIGLCFFITTTVAFPSGWTNAATFYGGSDASGTGACGYNLYATGY 60
      1  MKKIMLVLSLIGLCFFITTTVAFPSGWTNAATFYGGSDASGTGACGYNLYATGY 60
Db      1  MKKIMLVLSLIGLCFFITTTVAFPSGWTNAATFYGGSDASGTGACGYNLYATGY 60
QY      61  GRTTALSTALFNDGASCGQCYKIIDYKSDSFWCIKGSVYTTATNFCPPNLPNNNG 120
      61  GRTTALSTALFNDGASCGQCYKIIDYKSDSFWCIKGSVYTTATNFCPPNLPNNNG 120
Db      61  GRTTALSTALFNDGASCGQCYKIIDYKSDSFWCIKGSVYTTATNFCPPNLPNNNG 120
QY      121  GWCNPLKHPDMQAPAMEKIGIRGGIVPLFORVCKKGGVRFVNGDYELVLI 180
      121  GWCNPLKHPDMQAPAMEKIGIRGGIVPLFORVCKKGGVRFVNGDYELVLI 180
Db      121  GWCNPLKHPDMQAPAMEKIGIRGGIVPLFORVCKKGGVRFVNGDYELVLI 180
QY      181  VGGAGSIQSVFIKSGKTGMAMSRNMGWSNVAIYNGSLSPRVTTTGGETRFQDI 240
      181  VGGAGSIQSVFIKSGKTGMAMSRNMGWSNVAIYNGSLSPRVTTTGGETRFQDI 240
Db      181  VGGAGSIQSVFIKSGKTGMAMSRNMGWSNVAIYNGSLSPRVTTTGGETRFQDI 240
QY      241  VSWTFGGTSSPVQF 255
      241  VSWTFGGTSSPVQF 255
Db      241  VSWTFGGTSSPVQF 255
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QY 145 GlyGlyIleValProValIleuPheGlnArgValProCysIleValGlyValArg 164
Db 513 GGATGGCAATGTCCTGCTTACCAAGGATTCCTGGCAAAAAGGGGAGTTAGA 572
QY 165 PheSerValAsnGlyAAspTyrPheGlnIleuValIleuIleSerAsnValGlyValA 184
Db 573 TTCAACATAATGAGAGAACTATTGGAGCTATTGATGATTAACCAATGAGAGGGCT 632
QY 185 GlySerIleGlnSerValPheIleGlySerIleValGlyTyrMetAlaMetSerArg 204
Db 633 GGATCTGACATCTGTTCAATTAAGGCTCAAACTCAAACTGAGTACATGTCAGA 692
QY 205 AsnTyrGlnSerAsnTyrGlnSerAsnAlaTyrIleuAsnGlyIleuSerPheArg 224
Db 693 AATTGGGGGCAATTTGGCAATCCAAATGATCTCAATGGCCAACTGTTTAAAG 752
QY 225 ValThrThrAspGlyGlyIleuThrArgValPheGlnAspIleValProValSerTyrThr 244
Db 753 GTCAACATACCAACGGTGTCACTAAACATTTCTTAATGCTATCTCTCAACTGGAAT 812
QY 245 PheGlyIleuThrPheSerSerProValGlnPhe 255
Db 813 TTGGGCAACATATCACTTAAATTTTC 845
RESULT 15
AF332171 1031 bp mRNA linear PLN 23-APR-2004
LOCUS AF332171
DEFINITION Zea mays alpha-expansin 3 (expA3) mRNA, complete cds.
ACCESSION AF332171
VERSION AF332171.1 GI:14193754
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Wu, Y., Weeley, R.B. and Cosgrove, D.J.
TITLE Analysis and expression of the alpha-expansin and beta-expansin
gene families in maize
JOURNAL Plant Physiol. 126 (1), 222-232 (2001)
PUBMED 11351085
REFERENCE
AUTHORS Wu, Y., Weeley, R.B. and Cosgrove, D.J.
TITLE Direct Submission
JOURNAL Submitted (27-DEC-2000) Biology, Penn State University, 208 Mueller
Lab, University Park, PA 16802, USA
FEATURES
source
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/mol_type="mRNA"
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1..1031
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64..852
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/codon_start=1
/product="alpha-expansin 3"
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Alignment Scores: 1.83e-85 Length: 1031
Pred. No.: 1043.00 Matches: 186
Score:

Percent Similarity: 84.68% Conservative: 24
Best Local Similarity: 75.00% Mismatches: 38
Query Match: 74.34% Indels: 0
DB: 15 Gaps: 0
US-10-660-499a-2 (1-255) x AF332171 (1-1031)
QY 8 LeuGlySerIleuIleGlyLeuCyGpPheThrIleThrThrTyrAlaPheSerProSer 27
Db 103 CTGGCGTGTCTTGGGGCGGCTTCTCTGAGAGGACCGCGTCTTCTGGCGTCC 162
QY 28 GlyTyrPheAsnAlaIleAlaThrPheTyrGlyGlySerAspAlaSerGlyTyrMetGly 47
Db 163 GGAGTAAACAGCGCTTCCGACCTTCTATGGCGGTRGCCACGCTTCAGAAAGATGGGT 222
QY 48 GlyAlaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyrGlyThrArgThrAlaAlaLeu 67
Db 223 GGGGCTTGGGTACGGCAACGTGACTCGACGGGGTACGGACGGACGGCGGCGCTG 282
QY 68 SerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrIleIleCysAsp 87
Db 283 AGCAGCGCGCTCTTCAACGACGGCGCTCTGGGGGAGGCTAACCGGATCTCTGGAC 342
QY 88 TyrIleSerAspSerArgTyrCysIleGlyArgSerValThrValThrAlaAsn 107
Db 343 TACAGCGGACCCGCGGCTTCTGATCCGCGACGTCGATCACATCCGACCCACAC 402
QY 108 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeu 127
Db 403 CTGGCGCTTCCCAACTACCGCGCTGCGCAACGACGCGCGGTGTCACCGCGCGG 462
QY 128 LysHisPheAspMetAlaGlnProAlaTyrGlnIleGlyIleTyrArgGlyGlyIle 147
Db 463 CACACACTTCCACATGCGCGGCGCGCTGCTCAAGTCCGACATCACCGCGCGCATC 522
QY 148 ValProValIleuPheGlnArgValProCysIleValHisGlyGlyValAlaArgPheSerVal 167
Db 523 GTGCCGCTCAACTACCAAGAGGTGCGGTGTGAAGAAAGCGGGTGAAGTCAAGCATC 582
QY 168 AsnGlyAAspTyrPheGlnIleuValIleuIleSerAsnValGlyIleGlyIleSerIle 187
Db 583 AACGGGGCGCACTACTTCCAGCTGTCATCTCCAACTTCCGGCGGCTCGGGTCCATC 642
QY 188 GlnSerValPheIleGlySerIleValGlyTyrMetAlaMetSerArgAsnTyrGly 207
Db 643 CAGTCCGCTCCATCAAGGGGTGCGCACCGGGTGAATGCTCCCGAACTGGGGC 702
QY 208 SerAsnTyrGlnSerAsnAlaTyrIleuAsnGlyIleSerIleuSerPheArgValThrThr 227
Db 703 GTCAACTGGCACTCAACGCGTACCTCAATGGCCAGAGCTGTGTCAGATCACAGC 762
QY 228 ThrAspGlyGlyIleuThrArgValPheGlnAspIleValProValSerTyrThrPheGlyGln 247
Db 763 AGCGACGGCCAGACCAAACTTCCCGAGTGGCGCGCCGACGCTGGGGGTTCGGTCA 822
QY 248 ThrPheSerSerProValGlnPhe 255
Db 823 ACCTTTCGACCTCGCAGCATTC 846
Search completed: January 11, 2006, 22:55:10
Job time : 3868 secs

US-10-660-499a-2 (1-255) x AF291659 (1-1135)

QY 1 MetGlyLeu1leuLeuValleuGlySerLeu1leuGlyCys-----CysPheThr 18

Db 78 ATGCCATMAAAACAGAGTTTCATTACCACTTGGCTGCGAGCTTCTCTTTTGTCTCAGC 137

QY 19 lIethrThrThraAlaPheSerProSerGlyTTPThraAsnAlaHisAlaThrPheTyrgly 38

Db 138 ATTAACGCCAATGAGCTTCAACGGCTTCCGGTTGGAAGCTCAAGCCACCAACTTTTATGGA 197

QY 39 GlySerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyraAlaThr 58

Db 198 GCGAGGAGATGCTTCCGAAACAAATGGGTGGGCTGGGATGGGCAATTTGATCTGACT 257

QY 59 GlyTyrGlyThraThraAlaAlaSerThraAlaLeuPheAsnAspGlyAlaSerCys 78

Db 258 GGGTACGAAACAAACGGCTGCACTAAGACCGGCACTTTTCAACAATGGAGATGCTGC 317

QY 79 GlyGlnCysTyrllysIleIleCysAspTyrLysSerAspSerArgTTPCysIleTyrgly 98

Db 318 GGAACATGTTACAAAGATCAATGTGATTAACAAGCCGACCAACAATGGTCAGAAAGGT 377

QY 99 ArgSerValThraValThraAlaThraAsnPheCysProProAsnPheAlaLeuProAsn 118

Db 378 ACTTCGGTCACTATAACCGCACTAACTTCTGCCCCCAATTTGCTCTCCCGAACAT 437

QY 119 AsnGlyGlyTTPCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaTTPGlu 138

Db 438 AACGGGGGGGTGGTCAATCTCCGCGCCAGCACTTGGACATGGCTCAACCCGATGGCAG 497

QY 139 LysIleGlyIleTyraArgGlyGlyIleValProValLeuPheGlnArgValProCysLys 158

Db 498 AAGATGGCACTACACAAAGCGGSCATTTGTCGGCTTTTAAACAAACGAGCTTCAAG 557

QY 159 LysHisGlyGlyValArgPheSerValAsnGlyArgAspTyrPheGluLeuValLeuIle 178

Db 558 AAGCAGCGTGAAGTGAATTCACAGATCAACGGCAGACACTTCACTGATGCTTCAAGTC 617

QY 179 SerAsnValGlyIleGlySerIleGlnSerValPheIleGlySerIleTyrgly 198

Db 618 AGCAACGTGGAAACGCTGGTCCGTCAGATCTGTAATAAATCAAGGCTCAAAACAGAT 677

QY 199 TrpMetAlaMetSerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTyrlleuAsnGly 218

Db 678 TGGGTGACATGTCAGAACTGGGTGCTCTGGCAGCTTCACTTATCTCAACGCT 737

QY 219 GlnSerLeuSerPheArgValThrThraAspGlyIleThraArgValPheGlnAspIle 238

Db 738 CAATCTCTGCTTTATGTCACAAACAGATTTGCGTTCNMAAAACTCTTGAAGCTT 797

QY 239 ValProValSerTTPThraPheGlyGlnThraPheSerProValGlnPhe 255

Db 798 GTCCTCTTAATGAGGCTTTGGGACAGATTCATTCAGGCCAGTTCAGTT 848

RESULT 14

LOCUS AF049351 1334 bp mRNA linear PLN 23-APR-2004

DEFINITION Nicotiana tabacum alpha-expansin precursor (Nt-EXPA2) mRNA, complete cds.

ACCESSION AF049351

VERSION AF049351.1 GI:4027892

KEYWORDS

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

REFERENCE 1. Link, B.M. and Cosgrove, D.J. Acid-growth response and alpha-expansins in suspension cultures of bright yellow 2 tobacco Plant Physiol. 118 (3), 907-916 (1998)

JOURNAL PUBMED 9808735

REFERENCE 2 (bases 1 to 1334)

AUTHORS Link, B.M. and Cosgrove, D.J.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-1998) Biology, Pennsylvania State University, 208 Mueller Laboratory, University Park, PA 16802, USA

FEATURES

source location/Qualifiers

1..1334

/organism="Nicotiana tabacum"

/mol_type="mRNA"

/cultivar="Bright yellow 2"

/db_xref="taxon:4097"

/note="suspension culture"

1..1334

/gene="Nt-EXPA2"

78..848

/gene="Nt-EXPA2"

/function="involved in acid-growth response"

/note="cell wall protein"

/codon_start=1

/product="alpha-expansin precursor"

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/db_xref="GI:4027893"

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/note="predicted signal peptide"

150..845

/gene="Nt-EXPA2"

/product="alpha-expansin"

ORIGIN

Alignment Scores:

Pred. No.: 3,79e-86 Length: 1334

Score: 1052.00 Matches: 182

Percent Similarity: 83.67% Conservative: 28

Beet Local Similarity: 72.51% Mismatches: 41

Query Match: 74.98% Indels: 0

DB: 15 Gaps: 0

US-10-660-499a-2 (1-255) x AF049351 (1-1334)

QY 5 MetLeuValLeuGlySerLeu1leuGlyCysPheThrIleThrThraAlaPhe 24

Db 93 ATTTAGCAATGGGTTCAATTTGATTTGTAACCTTTTTCATGCAATGGTTTC 152

QY 25 SerProSerGlyTTPThraAsnAlaHisAlaThrPheTyrglyGlySerAspAlaSerGly 44

Db 153 TCTGCTTCTGGATGGAGAGTGTCTATGCACTTTTATGTTGAGACTATGCTTGTGG 212

QY 45 ThrMetGlyGlyAlaCysGlyTyrglyAsnLeuTyraAlaThrGlyTyrglyThraArgThr 64

Db 213 ACAATGGGGGTGCTTGGAGATATGGAATTTGTATATCAACAGGCTATGTAACAACT 272

QY 65 AlaAlaLeuSerThraAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrllysIle 84

Db 273 GCTGCACTTGAATACATGCACTTTTCAACAGATGAGATCAATGTGTAATGTTACAGAT 332

QY 85 IleCysAspTyrLysSerAspSerArgTTPCysIleTyrglyArgSerValThraValThr 104

Db 333 ATGTGATGTTACAAAGATCTTAATGTGTGAGAAAGAAACAAATGTTACAAATTAAC 392

QY 105 AlaThraAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTTPCysAsn 124

Db 393 GCCACAAATTTTGTCCACCAATTAATGCACTTCTTAAGCAACATGTGTGATGTGCAT 452

QY 125 ProProLeuLysHisPheAspMetAlaGlnProAlaTTPGluTyrllysIleTyrgly 144

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ORIGIN

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Percent Similarity:	84.46%	Conservative:	27
Best Local Similarity:	73.71%	Mismatches:	39
Query Match:	76.27%	Indels:	0
DB:	15	Gaps:	0

US-10-660-499a-2 (1-255) x AF049350 (1-1307)

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DB 103 ATTTAGCATTTGGTGTGATATTTGCAATTTTGTAAACCAATTTTTCAGTCGAAATGTTTC 162

QY 25 SerProSerGlyTrpThrAsnAlaHisAlaThrPheTrpGlySerAspAlaSerGly 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 163 TCTGCTTCTGATGCGACAGAGTCTCATGCCATTTTATGATGATCTGATCTTCTGCG 222

QY 45 ThrMetGlyGlyAlaCySeGlyTrpGlyAsnLeuTrpAlaThrGlyTrpGlyThrArgThr 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 ACTATGGGGGGTCTTGTGATATGAAATTTGTATTCACAGGGGATGGTACAAACACT 282

QY 65 AlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCySeGlyGlnCyTrpValIle 84
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DB 283 GCTGCAATTAAGTATGATGATTTGTCACAGATGAGATCTGTCGCAATGTTTCACATC 342

QY 85 IleCyAspTrpTrpSerAspSerArgTrpCySeIleLeuGlyArgSerValThrValThr 104
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DB 343 ATGTGTATTAACATCAAGATCTTAATGTGCGAAAGGAAACATATGTTACATTTACA 402

QY 105 AlaThrAsnPheCySeProAsnAspAlaLeuProAsnAsnAsnGlyGlyTrpCyAsn 124
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QY 125 ProProLeuTrpHisPheAspMetAlaGlnProAlaTrpGluValIleGlyIleTrpArg 144
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QY 145 GlyGlyIleValProValLeuPheGlnArgValProCySeIleValGlyValArg 164
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DB 523 GGTGTATTTGTTCTGCTCTCTATCAAGATTCCTGCGGAAAGGATGGAGTTTGA 582

QY 165 PheSerValaenglyArgAspTrpPheGluLeuValleuIleSerAsnValGlyVala 184
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QY 185 GlySerIleGlnSerValPheIleValGlySerIleTrpMetAlaMetSerArg 204
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QY 205 AsnTrpGlySerAsnTrpGlnSerAsnAlaTrpLeuAsnGlyGlnSerLeuSerPheArg 224
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QY 225 ValThrThrThrAspGlyGluThrArgValPheGlnAspIleValProValSerTrpThr 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 763 GTCACTACTACCGAGGGGTGTCACAAACATTTCTTAATGTTGTCTTCCAACTGGCA 822

QY 245 PheGlyGlnThrPheSerSerProValGlnPhe 255
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DB 823 TTTGGGAGACATATTCAACCTCTATTAATTTTC 855

RESULT 12
AC146790 114449 bp DNA linear PLN 22-JUN-2004
LOCUS Medicago truncatula clone mth2-123b21, complete sequence.
AC146790
ACCESSION AC146790

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VERSION

AC146790.16 GI:49034974

KEYWORDS

HTG. Medicago truncatula (barrel medic)

SOURCE

Medicago truncatula

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 114449)

AUTHORS

Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.

TITLE

Medicago truncatula BAC Clone mth2-123b21

JOURNAL

Unpublished

AUTHORS

Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.

TITLE

Direct Submission

JOURNAL

Submitted (07-OCT-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

REFERENCE

3 (bases 1 to 114449)

AUTHORS

Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.

TITLE

Direct Submission

JOURNAL

Submitted (12-JUN-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

REFERENCE

4 (bases 1 to 114449)

AUTHORS

Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.

TITLE

Direct Submission

JOURNAL

Submitted (22-JUN-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

COMMENT

On Jun 22, 2004 this sequence version replaced gi:48675415.

TITLE

Genome Center

JOURNAL

Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

FEATURES

Location/Qualifiers
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/clone="mth2-123b21"
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ORIGIN

Alignment Scores:
Pred. No.: 3.33e-85 Length: 114449
Score: 1067.50 Matches: 221
Percent Similarity: 43.04% Conservative: 17
Best Local Similarity: 39.96% Mismatches: 17
Query Match: 76.09% Indels: 298
Gaps: 2

ORIGIN

US-10-660-499a-2 (1-255) x AC146790 (1-114449)

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QY 1 MetGlyValleuMetLeuValleuGlySerLeuIleGlyLeuCySePheThrIleThr 20
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DB 5656 ATGACCAAGTTAATGTTATTTTGGGACACATGAGCTATGTTTTCACAAATAT 5715

QY 21 ThrTrpAlaPheSerProSerGlyTrpThrAsnAlaHisAlaThrPheTrpGlySer 40
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DB 5716 TCTTATGCTTCAAGCTTCTGATGACCAATGCTCATGCACTTTTATGGGGGATG 5775

QY 41 AspAlaSerGlyThrMet 46
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DB 5776 GATCGGAGGCACTATGAGTAAAGCCCTTGTACACCACTTTTCAACATTTATTCTAG 5835

QY 46 ----- 46

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Yamada,K. (SSP/PBEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PBEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

source

1. 1088

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/mol_type="mRNA"

/db_xref="taxon:3702"

/chromosome="1"

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/ecotype="Columbia"

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gene

1. 1088

/gene="Atlg20190"

misc_feature

42. 799

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/evidence=experimental

misc_difference

117. 118

/gene="Atlg20190"

/note="compared to genomic sequence"

misc_difference

812

/gene="Atlg20190"

/note="not present in genomic sequence"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

15

Gaps:

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1,74e-88

1076.50

86.33%

76.95%

76.73%

Length:

Matches:

Conservative:

Mismatches:

Indels:

1088

197

24

32

4

US-10-660-499a-2 (1-255) x AY080738 (1-1088)

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QY      20  ThrThrTyralaPheSerProSerGlyTTPThraAnaIahIaIaThrPheTyGlyGly 39
DB      90  GCGGTGATGCGCTTAGCGCTTCGCTTA-ACThaTGTCACGCTACATTTCTATGAGCA 148
QY      40  SerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyGlyAsnLeuTyralaThrGly 59
DB      149  AGTGAACGCTTCTGGAACAAATGGGTGAGCTTGCTTACGGAATCTTTACTCGCGGGG 208
QY      60  TyTGlyThraArgThraIaaIaLeuSerThraIaLeuPheAnaPglYalaSerCysGly 79
DB      209  TACGGGCAATGACGGCGGCTTAAGCAGCGCTGTTCACACGAGAGCTTCTTGGGA 268
QY      80  GluCysTyTrpIleIleCysAspTyTrpSerAspSerArgTrpCysIleGlyArg 99
DB      269  GAATGCTATAGATTAAGTGTGATCAAGCGGAGCTCAAGGTGTCTTGAAAGAGCT 328
QY      100  SerValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsn 119
DB      329  TCTGTGGTATTATACAGCACTAACTTTGGCCACCAACTTGTGCTTGGCTTAACAAC 388
QY      120  GlyGlyTTPCysAsnProProLeuLeuHisPheAspMetAlaGlnProAlaTTPGlyGly 139
DB      389  GGTGGTGTGTCATTCGCGCTTAAACATTTCACATGCAACACCGGCTTGGGAAG 448
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QY      140  ILGGLYIETyArgGlyGlyIleValProValLeuPheGlnArgValProCysGlyLeu 159
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QY      160  HisGlyValaArgPheSerValaAngIaArgAspTrpPheGlyLeuValleuIleSer 179
DB      509  AAGAGAGAGTATGATTCAGAAATTAACGGAAGAGACTTCCAGCTAGAGAAATATTCAA 568
QY      180  AsnValGlyValaGlySerIleGlnSerValPheIleGlySerIleThrGlyTTP 199
DB      569  AATGTAGAGAGACAGGTTTATTAATCTGTATTCATCAAGAGATCAAGAGCTGTTGG 628
QY      200  MetAlaMetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaTyLeuAsnGlyGln 219
DB      629  TTAGCCATCTCTGTAACCTGGAGAGCTAATTTGGCAATCGAATCTTATCAAGATGCTCAA 688
QY      220  SerLeuSerPheArgValThrThrThrAspGlyGlyThrArgValPheGlnAspIleVal 239
DB      689  GCTCTCTCTTTCACATTAACCACTAGATGAGTGTACTAGAGCTTTCATGATTTGTT 748
QY      240  ProValSerTrpThrPheGlyGlnThrPheSerSerProValGlnPhe 255
DB      749  CTTCTCTTGTGCTTTTGGACAGATTATTTCCACAGTTCAAGTT 796
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RESULT 11

AF049350

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Nicotiana tabacum (common tobacco)

Nicotiana tabacum

Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1307)

Link,B.M. and Cosgrove,D.J.

Acid-growth response and alpha-expansins in suspension cultures of

bright yellow 2 tobacco

Plant Physiol. 118 (3), 907-916 (1998)

9808735

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/organism="Nicotiana tabacum"

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/cultivar="Bright Yellow 2"

/db_xref="taxon:4097"

/note="suspension culture"

1. 1307

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88. 858

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QY	188	GInSeRValPheIleYegIYSerPYSThrgIYTPMeTAlaMeSerSerGAsnTrpGIY	207
Db	553	AAATCTGATTCATCAAAAGATCAAAAGACTGGTGGTATGAGCATGTCTGTAACTGGGGA	612
QY	208	SeRAnTTPGInSeRAsnAlaTYrIleuAnGIGInSeRLeuSeRPhaRgValThrThr	227
Db	613	GCTAATTGGCAATCGAATGCTTATCTTAAGATGGTCAAGGCTCTCTCTTCCATTACACT	672
QY	228	ThRaSPGIYGIuThARgValPheGInAsnIleValProValSerTrpThrPheGIYGIIn	247
Db	673	ACTAGTAGTGACTAGAGACTCTTCTGCATAGTGTGCTCTCTCTGAGCTTTGGACAG	732
QY	248	ThRPeSeRSeRProValGInPhe	255
Db	733	ATTATATCTTCCAAAGTTCAGTTT	756

RESULT	8
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LOCUS	1133 bp mRNA linear PLN 24-DEC-2002
DEFINITION	Capsicum annum putative expansin (upa7a) mRNA, complete cds.
ACCESSION	AF992631
VERSION	AF992631.1 GI:20149055
KEYWORDS	.
SOURCE	Capsicum annum
ORGANISM	Capsicum annum

REFERENCE
AUTHORS
TITLE
The xanthomonas type III effector protein AvrBs3 modulates plant

JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
host	expression and induces cell hypertrophy in the subseptal						
Mol. Plant Microbe Interact.	15 (7), 637-646 (2002)						
12118879							
2 (bases 1 to 1133)							
Marols, B., van den Ackerveken, G. and Bonas, U.							
Direct Submission							
Submitted (15-MAR-2002) Genetics, Martin-Luther University,							
Weinbergsweg 10, Halle 06099, Germany							
Location/Qualifiers							
1. .1133							

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Query Match:	77.66%
DB:	15
Length:	1133
Matches:	191
Conservative:	32
Mismatches:	32
Indels:	1
Gaps:	1

US-10-660-499A-2 (1-255) x AF492631 (1-1133)

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Db 54 ATGGCTAAATATTGATATTTTATTCGACTTGGGCTTTATATTTGGTTATTTAAACATTTCGCTT 113

QY 20 ThrThrTyraIaphSerProSerGlyYTrpThrAnaIahisAlaThrPheTyrgIyGly 39

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QY 40 SerAspAlaSerGlyThrMetGlyValaCySgIyTyrgIyAenLeuTyraIaThrGly 59

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QY 60 TyrgIyThrAgThrIaIaIaLeuSerThrIaIaenPheAnaPglYAlaSerCySgIy 79

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QY	100 SerValThrValThrIalThrAsnPhcCyproProbaenPhealaLeuproAasn	119
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QY	120 GtGtYTrPCyaaenProProleuLysiaPheaSpMetlaaginProalatrPGuLys	139
Db	414 GGTCGATGGTGTTATCTCCCAAGGCCCAATTTTGACATGGCTCAACCCTGCTGGGAACAC	473

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Db	774	TCATCCAAATTGGCAATTTGGGCAACATATTCAGCTCTATGAACTTC	821
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LOCUS	AF049352	1174 bp	mRNA
DEFINITION	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA3)		mRNA,
ACCESSION	AF049352		complete cds.
VERSION	AF049352.1	GI:4027894	
KEYWORDS			
SOURCE	Nicotiana tabacum (common tobacco)		
ORGANISM	Nicotiana tabacum		

REFERENCE
AUTHORS
TITLE
JOURNAL

Link, B.M. and Cosgrove, D.J.
Acid-growth response and alpha-expansins in suspension cultures of
bright yellow 2 tobacco
Plant Physiol. 118 (3), 907-916 (1998)

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Qy 88 TyrLysSerAspSerArgTrpCysIlelysglyArgSerValThrValThrAlaThrAsn 107
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Qy 128 LysHisPheAspMetAlaGlnProAlaTTPGluVlyIleGlyTyrArgGlyGlyIle 147
Db 373 AAACATTTGACATGACACACCCGCTTGAAAAGATGGAATTTACAGAGAGCAATC 432
Qy 148 ValProValLeuPheGlnArgValProCysLysLysHisGlyValArgPheSerVal 167
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Qy 168 AengIyArgAspTyrPheGluLeuValLeuIleSerAsnValGlyValAlaGlySerIle 187
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Qy 188 GlnSerValPheIlelysglySerLysThrGlyTyrMetAlaMetSerArgAsnTTPGly 207
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RESULT 7
LOCUS AF332436 759 bp mRNA linear PLN 07-MAY-2003
DEFINITION Arabidopsis thaliana clone C00124 (e) putative expansin S2
ACCESSION AF332436
VERSION AF332436.1 GI:12083279
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eumariophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 759)
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.,
Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shim, P., Southwick, A.,
Tripp, M.G., Wu, T., Davis, R.W., Becker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) clones
Unpublished
2 (bases 1 to 759)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P.,
Lee, J.M., Toriumi, M., Yu, G., Brooker, S., Chao, Q., Chen, H.,
Karlin-Neuman, G., Kim, C., Lam, B., Miranda, M., Nguyen, M.,
Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Becker, J.R. and
Theologis, A.
Direct Submission
Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 759)
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.,
Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shim, P., Southwick, A.,
Tripp, M.G., Wu, T., Davis, R.W., Becker, J.R. and Theologis, A.
Direct Submission
Submitted (07-MAY-2003) Plant Gene Expression Center, 800 Buchanan

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COMMENT
Annotation based on July 2002 version of the Arabidopsis genome
submitted to Genbank.
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ORIGIN
Alignment Scores:
Pred. No.: 5 37e-90 Length: 759
Score: 1091.00 Matches: 195
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Best Local Similarity: 78.63% Mismatches: 33
Query Match: 77.76% Indels: 0
DB: 15 Gaps: 0
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Qy 68 SerThrAlaLeuPheAsnAspIleAlaSerCySPGlyGlnCySPyTyrIleIleCySPAsp 87
Db 193 AGCAGCGCTCTTTCAACAGCAGAGCTTCTCGGAGATGCTATAGATTAACGTGTGAT 252
Qy 88 TyrLysSerAspSerArgTrpCysIlelysglyArgSerValThrValThrAlaThrAsn 107
Db 253 CACGGCGCGGACTCTACCGGTCGCTTGAAAGAGCTTCGTGTATTACACCACTAAC 312
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Qy 128 LysHisPheAspMetAlaGlnProAlaTTPGluVlyIleGlyTyrArgGlyGlyIle 147
Db 373 AAACATTTGACATGACACACCCGCTTGAAAAGATGGAATTTACAGAGAGCAATC 432
Qy 148 ValProValLeuPheGlnArgValProCysLysLysHisGlyValArgPheSerVal 167
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REFERENCE
1 asteride; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS
Vogler H. and Mandel T.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1318)
AUTHORS
Vogler H.
TITLE
Direct Submission
Submitted (05-MAY-2003) Vogler H., Biology, University of Berne,
Altengeryrain 21, Berne, 3013, SWITZERLAND
JOURNAL
Location/Qualifiers
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ORIGIN

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Query Match: 77.98% Indels: 2
DB: 15 Gaps: 2

US-10-660-499a-2 (1-255) x LBSS560646 (1-1318)

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QY 20 ThrThr--TyrAlaPheSerProSerGlyTTPThraAlaHisAlaThrPheYrgly 38
DB 131 AGTACTGCAAAATGCTTCTGCTTCTGATGATGATGATGATGATGATGATGATGATG 190
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DB 251 GGTATAGGACCAACACTGCTGCAATTAAGTACATGTCATGTCATGATGAGCATCATGT 310
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QY 139 LysIleGlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysLys 158
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LOCUS
Sequence 2291 from Patent WO2004035798.
DEFINITION
CQ805880
ACCESSION
CQ805880.1 GI:47111574
VERSION
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1 Inze, D., de Veylder, L. and Vlieghe, K.
AUTHORS
Identification of novel e2f target genes and use thereof
TITLE
Patent: WO 2004035798-A 2291 29-APR-2004;
JOURNAL
CropDesign N.V. (BB)

FEATURES

source
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ORIGIN

Alignment Scores:

Pred. No.: 5.37e-90 Length: 759
Score: 1091.00 Matches: 195
Percent Similarity: 86.69% Conservative: 20
Best Local Similarity: 78.63% Mismatches: 33
Query Match: 77.76% Indels: 0
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US-10-660-499a-2 (1-255) x CQ805880 (1-759)

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QY 28 GlyTTPThraAlaHisAlaThrPheTyrGlyLysSerAspAlaSerGlyThrMetGly 47
DB 73 GGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 132
QY 48 GlyAlaCyseGlyTyrGlyAsnLeuYrAlaThrGlyTyrGlyThrArgThrAlaAlaLeu 67
DB 133 GGAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 192
QY 68 SerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrLysIleLysCysAsp 87
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QY      123 CysAsnProProLeuIleYsgIlePheAspMetAlaGlnProAlaTyrPheGluIleGlyIle
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QY      163 ValArgPheSerValAsnGlyArgAspTyrPheGluIleuValIleuIleSerAsnValGly
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QY      223 PheArgValThrThrThrAspGlyIleThrArgValPheGlnAspIleValProValSer
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QY      243 TyrThrPheGlyIleThrPheSerSerProValGlnPhe
Db      771 TGGAAATTTGGCCAAACATTTTCAAGCAAAATCTCAATTC
RESULT 3
CSU30460
LOCUS   Cucumis sativus expansin S2 precursor (Cs-EXPA2) mRNA, complete
DEFINITION
ACCESSION   U30460.1
VERSION     GI:1040876
KEYWORDS
SOURCE      Cucumis sativus (cucumber)
ORGANISM    Cucumis sativus
REFERENCE   1 (bases 1 to 1366)
AUTHORS     Sheherbati,Y., Shi,J., Durachko,D.M., Gullitman,M.J.,
            McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.
TITLE       Molecular cloning and sequence analysis of expansin--a highly
            conserved, multigene family of proteins that mediate cell wall
            extension in plants
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)
PUBMED     7568110
REFERENCE   2 (bases 1 to 1366)
AUTHORS     Sheherbati,Y., Shi,J., Durachko,D.M., Gullitman,M.J.,
            McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.
TITLE       Direct Submission
JOURNAL     Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania
            State University, 208 Mueller Laboratory, University Park, PA
            16802, USA
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ORIGIN

Alignment Scores:

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Best Local Similarity:	81.25%	Mismatches:	1
Query Match:	78.65%	Indels:	1
DB:	15	Gaps:	1

US-10-660-499a-2 (1-255) x CSU30460 (1-1366)

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Db      346 TATGGCAGAGCGATGCTCTGGACAAATGGGTGGAGCTTGTGGATGGAACCTTAATAC
QY      57 AlaThrGlyTyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAla
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QY      77 SerCysGlyIleCysEtyIleIleIleCysAspTyrIleSerAspSerArgTyrCysIle
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QY      97 LysGlyArgSerValThrValThrAlaThrAsnPheCysProProAsnPhelaleuPro
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QY      157 CysIleYsgIleGlyIleValArgPheSerValAsnGlyArgAspTyrPheGluIleuVal
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QY      177 LeuIleSerAsnValGlyIleValIleGlnSerValPheIleYsgIleYsgIleYsg
Db      766 CTATATACCAACGATGGGAGAGGGGTGACATCACTGATGCTTATTAAGGCTCTTAA
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ORIGIN

Alignment Scores:

Pred. No.: 3.29e-118 Length: 1089
Score: 1403.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-660-499a-2 (1-255) x AFS16879 (1-1089)

QY 1 MetG1VLYe11eMeLeuVal1eug1ySer1eul1eG1yLeuCy6Cy8pHeThr11eThr 20
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QY 21 ThrTyrAlaPheSerProSerG1yTyrThrAsnAlaHisAlaThrPheTyrG1yG1ySer 40
DB 112 ACCATAGCCTTCTCACCTTGTGATGGACCAAGCCCATGCCATTTTATGGGGGTAGT 171
QY 41 AspAlaSerG1yThrMetG1yG1yAlaCy6G1yTyrG1yAsnLeuTyrAlaThrG1yTyr 60
DB 172 GAATGCTTCAGAACTATGGGGGAGCTTGAGGATGGAAATCTGATGCACTGGGAT 231
QY 61 G1yThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspG1yAlaSerCy6G1yG1n 80
DB 232 GGAACCTAGAACCTGACGCTTAAAGACGCTTATTTATATGAGGCTTCTGTGGTCA 291
QY 81 CysTyr1y1e11e1yCy6AspTyr1y1ySerAspSerArgTyrCy61y1yG1yG1ySer 100
DB 292 TGGTCAAAATTTATATGATTTACAAATCAGACTCTGATGCTGCATCAAAAGGAATCT 351
QY 101 ValThrValThrAlaThrAlaPheCysProProAsnPheAlaLeuProAsnAsnG1y 120
DB 352 GTAAACGGTAACCTGCAAACTTTTGCCTCCCAATTCGCCCTTCTTAACAAATGGA 411
QY 121 G1yTyrCy6AsnProProLeu1y1yPheAspMetAlaG1nProAlaTyrG1yG1y1e 140
DB 412 GGGTGGTGAACCAACCACTCAAGCATTTGATATGAGCCCAACCCGTTGGAAAAATTT 471
QY 141 G1y1y1eTyrArgG1yG1y1y1eValProVal1y1yPheG1nArgVal1yProCy61y1yG1yHis 160
DB 472 GGTATTTACAGAGGAGGATCGTCCCGTCTAATTTCAAAAGGTTCCATCAAAACAT 531
QY 161 G1yG1yValArgPheSerValAsnG1yArgAspTyrPheG1yLeuVal1y1ySerAsn 180
DB 532 GGAAGGGTGAAGTTCAGTGAATGGAAGGAGCATTTGAGCTAGATGATCAGCAAT 591
QY 181 ValG1yG1yAlaG1ySer1y1yG1nSerValPhe1y1yG1yG1ySer1y1yThrG1yTyrMet 200
DB 592 GTGGGGGCTGCTGATCATTCAATCAGTGTCTTAAAGGCTCAAAAGCTGATGATG 651
QY 201 AlaMetSerArgAsnTyrG1ySerAsnTyrG1nSerAsnAla1y1yLeuAsnG1yG1nSer 220
DB 652 GCATATGCAAGAAATTTGGGGTCTTAATTTGGCAATCCATGCGTATTTTGAATGGCAATCT 711
QY 221 LeuSerPheArgVal1yThrThrThrAspG1yG1yThrArgVal1yPheG1nAsp1y1eValPro 240

DB 712 TTGTCCTTACAGGGTCAACCACTGATGAGAGACCAAGATTTTCCAGATATGTTCCA 771
QY 241 ValSerTyrThrPheG1yG1nThrPheSerSerProValG1nPhe 255
DB 772 GTAAGTTGACATTCGGCCAACTTTCTTACGCCCATTCAGTTTCAGTTTC 816

RESULT 2

AF184232

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

PUBMED

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ORIGIN

Alignment Scores:

Pred. No.: 1.42e-91 Length: 1103
Score: 1110.50 Matches: 195
Percent Similarity: 88.14% Conservative: 28
Best Local Similarity: 77.08% Mismatches: 29
Query Match: 79.15% Indels: 1
DB: 15 Gaps: 1

US-10-660-499a-2 (1-255) x AF184232 (1-1103)

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DB 51 GTCAATTTAGCATTTGGATTTTAAATTTGTTTGTTGATGATTTTCTTCAGTGAATGAT 110
QY 24 PheSer---ProSerG1yTyrThrAsnAlaHisAlaThrPheTyrG1yG1ySerAspAla 42
DB 111 TTCTCAGCAGATTCGATGAGCAAGGCTCATGCCCATTTATGCTGAGCTGATGCT 170
QY 43 SerG1yThrMetG1yG1yAlaCy6G1yTyrG1yAsnLeuTyrAlaThrG1yTyrG1yThr 62
DB 171 TCGGCGCAATGGAGGTGCTTGAGTATGATGATTTGATTTGATTCACAGATATGATCT 230
QY 63 ArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspG1yAlaSerCy6G1yG1nCy6Tyr 82

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2006, 21:08:50 ; Search time 3843 Seconds
(without alignments)
3771.814 Million cell updates/sec

Title: US-10-660-499a-2

Perfect score: 1403
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O/cgcn2.1/USPTO.spool_p/US1060499/runat.10012006.105620.16422/app.query.fasta_1.391
-DB=GenEmbl -QFMT=faaext -SUFRTX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEJOURN -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

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2: gb_in:*
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4: gb_om:*
5: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	100.0	1089	15	AF516879 Glycine m
2	1110.5	79.2	1103	15	AF184232 Lycopersi
3	1103.5	78.7	1366	15	CSU30460 Cucumis sat

4	1098.5	78.3	978	15	AY084514 Arabidops
5	1094	78.0	1318	15	LBES560646
6	1091	77.8	759	6	CQ805880 Sequence
7	1091	77.8	759	15	AF332436 Arabidops
8	1089.5	77.7	1133	15	AF492631 Capsicum
9	1087	77.5	1174	15	AF049352 Nicotiana
10	1076.5	76.7	1088	15	AY080738 Arabidops
11	1070	76.3	1307	15	AF049350
12	1067.5	76.1	11449	15	AC146790
13	1066	76.0	1135	15	AF291659
14	1052	75.0	1334	15	AF049351
15	1043	74.3	1031	15	AF332171
16	1039	74.1	1081	15	OSXEXPANSI
17	1039	74.1	1137	15	AK069548
18	1033.5	73.7	1355	15	AB196979
19	1029	73.3	92710	15	T20H2
20	1002	71.4	965	15	AY589583
21	993.5	70.8	2637	15	AF394543
22	993.5	70.8	110007	15	AP008210_085
23	993.5	70.8	150007	15	OSJN00248
24	987	70.3	1071	15	AK070133
25	977	69.6	708	15	DQ061068
26	971.5	69.2	789	6	AX653377
27	965.5	68.8	826	15	DQ061055
28	944	67.3	110000	15	AP008212_299
29	944	67.3	110000	15	AP008212_300
30	944	67.3	143507	15	AC091774
31	944	67.3	150660	15	AP003769
32	937	66.8	1132	15	AB196982
33	936.5	66.7	753	6	AX652920
34	936.5	66.7	1037	15	AY046929
35	930	66.3	1070	15	AY079208
36	928.5	66.2	850	15	DQ061064
37	920	65.6	895	15	DQ061063
38	918.5	65.3	1145	15	FP827606
39	916	65.1	1487	15	CAR489608
40	914	65.1	1497	15	AF085330
41	912.5	65.0	998	15	AF085330
42	909.5	64.8	891	15	PT064893
43	909.5	64.8	919	15	PT064891
44	907	64.6	1351	15	AY435101
45	906.5	64.6	860	15	DQ061065

ALIGNMENTS

RESULT 1
LOCUS AF516879 1089 bp mRNA linear PLN 19-MAR-2003
DEFINITION Glycine max expansin (EXPI) mRNA, complete cds.
ACCESSION AF516879
VERSION AF516879.1 GI:27464176
KEYWORDS
SOURCE Glycine max (soybean)
ORGANISM Glycine max
REFERENCE 1 (bases 1 to 1089)
AUTHORS Lee,D.K., Ahn,J.H., Song,S.K., Choi,Y.D. and Lee,J.S.
TITLE Expression of an Expansin Gene Is Correlated with Root Elongation
in Soybean
JOURNAL Plant Physiol. 131 (3), 985-997 (2003)
PUBMED 12644651
REFERENCE 2 (bases 1 to 1089)
AUTHORS Lee,D.-K., Ahn,J.H., Choi,Y.D. and Lee,J.S.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2002) School of Biological Sciences, Seoul
National University, Shinrim-dong, Kwanak-gu, Seoul 151-747, Korea
FEATURES
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Qy	120	GLYGLYTPCYASPnProProLeuLYbHisPheASPMeTAlaGlnProAlaTrpGluYr	139
Db	431	GGAGGGGTGGTGCAACCCACCCCTGCAGCAATTCGATATGCTCAGCAGCAATGGGAAAG	490
Qy	140	IllegiYleYrArGGLYGLYrIleValProValleuPheGlnArGValProCYbLYbLYs	159
Db	491	ATCGGATTATTCAGAGCGCGGAGTCGTCGCAAGTCCTTTCCAAAGGTTCCATGTAAAG	550
Qy	160	HisGLYGLYValArGSPheSeArValaengIYArGASPTrPheGlnuLeuValleuIleSer	179
Db	551	CATGTGGTGTTAGATTCAGTGTATATGAGAGACACTCTCCAAATGATTGATTAAGC	610
Qy	180	AsnValGLYGLYAlaGLYSerIleGlnSerValPheIleLYbSglYSerLYsTrhGlyYTP	199
Db	611	AATGTAGCTGGGGCTGGATCTAATTCATACATCAATCAATCAAGAGCTCCGGACCAATTGG	670
Qy	200	MeTAlaMeTSeArArGAsnTrpGLYSeArAsnTrpGlnSerArSnaAlaTrYrleuAengIYgln	219
Db	671	ATGGCCATGTCCAGGAACTGGGAGGACTTACTGGCACTTAATCCATATCCATATGCGCCAG	730
Qy	220	SeArLeuSerPheArGValThrThrThraSPGLYGLUThArGValaPhe	235
Db	731	TCTGTGTCCTTCAGAGTCAACCACTGATGATGAGTCAACCCAAATATTC	778

FEATURES	REFERENCE	TITLE	JOURNAL	COMMENT
LOCUS	CE208602			
DEFINITION	CE208602			
ACCESSION	CAB20003_1va_F09			
VERSION	CAB20003_1va_F09			
KEYWORDS	EST			
ORGANISM	Vitis vinifera			
SOURCE	Vitis vinifera			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.			
	1 (bases 1 to 777)			
	Goes da Silva,F., Indolino,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D.			
	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages			
	Unpublished (2003)			
	Contact: Douglas Cook, Phd			
	CABE Genome Facility			
	UC Davis, Plant Pathology			
	One Shields Ave, Davis, CA 95616, USA			
	Tel: 530 754 6561			
	Fax: 530 754 6617			
	Email: drcoc@ucdavis.edu			
	Seq primer: ACGGTACCGACATATGCC.			
	Location/Qualifiers			

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/sex="Heraphrodite"
/dec_stage="Bloom"
/clone_lib="Cabernet Sauvignon flower bloom - CAB2"
/site="Organ: Flower - Bloom; Vector: pDNR; Site: 1: 5'UTR;
note=2: 3'UTR; CAB2 is a cDNA library of Vitis vinifera cv

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ORIGIN

Alignment Scores:

Pred. No.:	4.04e-107	length:	777
Score:	1081.50	Matches:	196
Percent Similarity:	90.91%	Conservative:	14
Best Local Similarity:	84.85%	Mismatches:	20
Query Match:	77.08%	Indels:	1
DB:	6	Gaps:	1

US-10-660-499A-2 (1-255) x CF208602 (1-777)

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Oy      1 MetGlySerIleMetIeu---ValIeuGlySerIleIleGlyLeuCySCysPheThrIle 19
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      81 ATGGCGAAAATCTGCTTCAATGCTTTAGCAATGTCGCGGTAATTGCTATTTTCTCG 140

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Qy 20 ThrThrTyraIapheserProserGlyTyrPhrAsnaIahSsaIathrPherGlyGly 39
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Qy      40 SerSPALSerglyThmetglylAlaCysglyTyrGlyAsnLeuTyrAlaThGly 53
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Oy TyrglyThraargThraIaaIeuserThraIaleupheasnaapcyalaaserCysely 79
 Db 261 TATGAAACAAGAACGCGACGCTTTGAGCACAGCATTGTTCAATGATGGGGCTTCATGTGGG 320

Qy 80 GlnCysTyrIleSileIleCysAspTyrLysSerAspSerArgTyrCysIleLysGlyArg 99
 |||||
 Db 321 CAAAGCTACAGATCATATGTGATTACCAATCCGATTCAAGTGTTCAGAAAGGAGCT 380

Qy 100 SerValThrValThAlaIAsnProCAsnPheAlaLeuProAsnAsnIsn 115
| | | | | : : : | : : : | : : : |
Db 381 TCTGTGACCATCACTGCACAACACTTTGGCCCTCCAACATACTGCTCTTCCAGCAACAT 440

Qy 120 GAGGCTGCGACCCACCCTGAGCATTCGATTGGCTCAGCGAGCATGGGAAAG 500
 Db 441 GAGGCTGCGACCCACCCTGAGCATTCGATTGGCTCAGCGAGCATGGGAAAG 500

Db 501 ATCGGATTACAGAGCGGATCGTCCAGTGTTCAAAGGGTTCATGTAAAGAG 566

160 HIBGGYGLVVALATPnesetvalaanglYalgaBpyLIFneGluDeuvalDeuLresel
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QY 172 TyrPheGlnLeuValLeuIleSerAsnValGlyValaGlySerIleGlnSerValPhe 191
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|||
Db 422 TACTGCAATTAAGATTGATTAAGCAATGACGCTGGAGCTGATCTATTCATCAATCA 481
QY 192 IleGlyGlySerIleThrGlyTyrMetAlaMetSerArgAsnTrpGlySerAsnTrpGln 211
|||
|||
Db 482 ATCAAGGCTCCGGACCAAGTTGGATGGCCATGTCCAGAACTGGGAGCTTAAGTCCAG 541
QY 212 SerAsnAlaTyrLeuAsnGlyGlnSerLeuSerPheArgValThrThrAspGlyGln 231
|||
|||
Db 542 TCTAATGCTCATCTCAATGCGCAGTCTCTCTTCAAGGTCAACACCTGATGAGTGC 601
QY 232 ThrArgValPheGlnAspIleValProValSerTyrPheGlyGlnThrPheSerSer 251
|||
|||
Db 602 ACCCAAGAAATTCAGCAATGTGTGCTTCAGATTGGGGGTTGGTCAACCTTCTTACG 661
QY 252 ProValGlnPhe 255
|||
|||
Db 662 TCAGTACAGTTT 673
RESULT 11
CX187525 832 bp mRNA linear EST 28-DEC-2004
LOCUS CX187525
DEFINITION 96-B0227270-021-012-023-frev ADIS-MP12 021 Brassica napus cDNA clone
ACCESSION CX187525
VERSION CX187525.1 GI:56834949
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS Jakoby, M., Lehmann, D. and Weisshaar, B.
TITLE Direct submission to GenBank (ADIS-MP12 021)
JOURNAL Unpublished (2004)
COMMENT Contact: Bernd Weisshaar
Chair of Genome Research
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Tel: +49-521-106 6873
Fax: +49-521-106 6423
Email: Bernd.Weisshaar@uni-bielefeld.de
Insert length: 832 Std Error: 0.00
Plate: 12 row: 0 column: 23
Seq primer: frey.
FEATURES
source location/Qualifiers
1. 832
/organism="Brassica napus"
/mol_type="mRNA"
/cultiivar="Express 617"
/db_xref="GABI:1119672"
/db_xref="taxon:3708"
/clone="MP12p102202312Q"
/issue="flowers and flower buds"
/tissue_type="flowers and flower buds"
/dev_stage="young flowers and flower buds"
/clone_11b="ADIS-MP12 021"
/note="Vector: pSPOR1; Site 1: SalI; Site 2: NotI; cDNA
library from Brassica napus, strain Express 617; RNA was
from young flowers and flower buds of two greenhouse
plants; library was made at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
SalI-NotI, primer sites and orientation:
T7-SalI-CCACGGCTCG-5'ccr-cDNA-polyA-CC-NotI-SP6; made by
Marc Jakoby 09/2000; PI: Bernd Weisshaar. Sequence
submission managed by KZPD/GABI-Primary database:
http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 1,93e-108 Length: 832
Score: 1094.00 Matches: 196
Percent Similarity: 86.69% Conservative: 19
Best Local Similarity: 79.03% Mismatches: 33
Query Match: 77.98% Indels: 0
DB: 8 Gaps: 0
US-10-660-499a-2 (1-255) x CX187525 (1-832)
QY 8 LeuGlySerIleuIleGlyLeuCysPheThrIleThrThrValaPheSerProSer 27
|||
|||
Db 28 CTAGCTGAGATTGGTGTCTTTGGCCGCTCTGTATATGCGGTGATGCGTTAGCCCTTC 87
QY 28 GlyTyrThrAsnAlaHisAlaThrPheTyrGlyGlySerAspAlaSerGlyTyrMetGly 47
|||
|||
Db 88 GGTTTAACAAATGGCCACCGCACATTTCTATGAGGAGTGAACCTTCTGGAACAAATGGC 147
QY 48 GlyAlaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyrGlyTyrThrArgThrAlaAlaLeu 67
|||
|||
Db 148 GGAGCTTGTGGTACGAGATCTCTACTCTGCGGGGTACCGGCAATGACGGCGGCTA 207
QY 68 SerThrAlaIleuPheAsnAspGlyAlaSerCysGlyGlnCysTyrIleIleCysAsp 87
|||
|||
Db 208 AGCAGCGCTCTGTTTAAACAGGAGCTTCTTGCGCGGAATGCTATAGATACGTCGAC 267
QY 88 TyrIleSerAspSerArgTyrPyrCysIleGlyArgSerValThrValThrAlaThrAsn 107
|||
|||
Db 268 TACGCGCGGACCTCAGGTGTGTCAAGAAAGAGCTTCGGTGTATACAGCAACCAAC 327
QY 108 PheCysProProAsnPheAlaIleuProAsnAsnAsnGlyGlyTyrPyrCysAsnProProLeu 127
|||
|||
Db 328 TTCGCCACCGAATCTTGGCTTCCCAACCAAGAGGTGGTGGTCAACCGCGCTC 387
QY 128 LysHisPheAspMetAlaGlnProAlaTyrPylulIleGlyIleTyrArgGlyGlyIle 147
|||
|||
Db 388 AAACATTTCCACATGGCACAAACCGCTTGGAGAAAGATCGGAATCTACAGAGCGGATC 447
QY 148 ValProValIleuPheGlnArgValProCysLeuGlyHisGlyValArgPheSerVal 167
|||
|||
Db 448 GTCCCGCTGCTGTCCAAAGATTAAGTTGTACAAAGAGAGAGATTCAGATC 507
QY 168 AsnGlyArgAspTyrPheGlnLeuValLeuIleSerAsnValGlyValaGlySerIle 187
|||
|||
Db 508 AACGGCAGGATTAATCTTCAAGTGAACATTTCCAACTGAGAGAGCTGGTTCAT 567
QY 188 GlnSerValPheIleGlySerIleThrGlyTyrMetAlaMetSerArgAsnTrpGly 207
|||
|||
Db 568 CAGTCTGTATCCATCAAGATCAAAACGTGTGTAGCTATGTCTCGTAACTGGGGA 627
QY 208 SerAsnTrpGlnSerAsnAlaTyrLeuAsnGlyGlnSerLeuSerPheArgValThrThr 227
|||
|||
Db 628 GCTAATTTGGCAATCAACGCTTATCTCGATGGCAATCTTTCTTCTTCATTAACAT 687
QY 228 ThrAspGlyGlnThrArgValPheGlnAspIleValProValSerTyrThrPheGlyGln 247
|||
|||
Db 688 ACCGATGTGTCTACGAGAGCTTCCCAAGTGTTCCTTCTGTGCTTTCGAGCAG 747
QY 248 ThrPheSerSerProValGlnPhe 255
|||
|||
Db 748 ACTTATCTTTCAGAAAGTTCAGTTT 771
RESULT 12
BE607657 617 bp mRNA linear EST 13-JUL-2004
LOCUS BE607657
DEFINITION eg15c07.y1 Gm-cl046 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl046-901 5' similar to TR:Q39626 Q39626 EXPANSIN S2 PRECURSOR.
/, mRNA sequence.
ACCESSION BE607657
VERSION BE607657.1 GI:9898689
KEYWORDS EST.

Score: 1096.00 Matches: 194
 Percent Similarity: 86.77% Conservative: 29
 Best Local Similarity: 75.49% Mismatches: 32
 Query Match: 78.12% Indels: 2
 DB: 2 Gaps: 2

US-10-660-499A-2 (1-255) x BG592843 (1-789)

```

QY 1 MetGlyLysIle--MetLeuValLeuGlySerLeuIleGlyLeuGlyCysPheThrIle 19
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 7 ATGGCCAAATATGGCATTTTAACTAGGTTTCATATTTGTTTGTGTAACATTTGGTT 66
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 20 ThrThr---TyrAlaPheSerProSerGlyTTPThraSpAlaIstAlaThrPheTyrGly 38
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 67 AGTACGCAATGCTCTCTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 126
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 39 GlySerAspAlaSerGlyThrMetGlyValAlaCysGlyTyrGlyValLeuLeuTyrAlaThr 58
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 127 GGAATCTGATGCTTCTGCGACAAATGGGGGCTTGGCTATGGCAATTTGATCTACACA 186
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 59 GlyTyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCys 78
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 187 GGTATAGTACAAACACTGCTGATTAAGTACGATTTGTCATGATGATGGCATCATGT 246
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 79 GlyGlnCysTyrLysIleIleCysAspTyrLysSerAspSerArgTTPCysIleGly 98
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 247 GGTCAATGTTACAAATATGATGATTAATCAAGATTTCTAAATGCTGATTAAGGGA 306
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 99 ArgSerValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsn 118
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 307 ACATCTAATTAACAAATTAAGTACGACCAATTTTGTCCAAATTTGCACTTCTAGCAAT 366
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 119 AsnGlyGlyTTPCysAsnProProLeuLysIlePheAspMetAlaGlnProAlaTTPGly 138
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 367 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 139 LysIleGlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysLys 158
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 427 CACATTTGATCTACAAAGGTGATGATTTCTGTCATGACCAAGATTTCTTGTGTG 486
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 159 LysHisGlyGlyValArgPheSerValAsnGlyValArgAspTyrPheGlyLeuValLeuIle 178
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 487 AAAAAAGGTGATGATTTTACAAATTAAGTAAAGGACATTTTGTGCTAATTAAGTAA 546
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 179 SerAsnValGlyValArgIleGlnSerValPheIleLysGlySerLysThrGly 198
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 547 AGCAATGATGAGAGGCTGATCAATTCATCAATTAAGTAAAGGTTTCAAGAACCAAT 606
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 199 TrpMetAlaMetSerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTyrLeuAsnGly 218
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 607 TGAATGCAATGCTAGAAATTTGGGGGCCAATTTGGCAATCAATGATTTCTTAATGGA 666
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 219 GlnSerLeuSerPheArgValThrThrThrAspGlyGlyIleThrArgValPheGlnAspIle 238
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 667 CAATCTTTGTCATTTAAGTCAACAACATGATGATGATGATGATGATGATGATGATGATGAT 726
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 239 ValProValSerTTPThrPheGlyGlnThrPheSerSerProValGlnPhe 255
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 727 GCTTCAATCCAAATTTGGCAATTTGGCAACATATTCAGCTCTATTAACCTTC 777
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

REFERENCE 1 (bases 1 to 760)
 AUTHORS Goes da Silva, F., Iandolo, A., Lam, H., Baek, J., Leslie, A., Xu, J.,
 Jones, K., and Cook, D.
 TITLE Expressed sequence tags from cabernet sauvignon berries at various
 developmental stages
 JOURNAL Unpublished (2003)
 COMMENT Contact: Douglas Cook, PhD
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcooc@ucdavis.edu
 Seq primer: ACGGTACCGGACATATGCC.
 Location/Qualifiers

FEATURES
 source 1..760
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB70004_IIIAF_H07"
 /sex="Hermaphrodite"
 /dev_stage="Post-Veraison, 18-19 brix"
 /lab_host="DH5alpha"
 /clone_11b="Cabernet Sauvignon Berry Post-Veraison - CAB7"

/note="Organ: Berry; Vector: pDKR; Site 1: Sfil; Site 2: 8
 Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8
 berries. Samples were collected post-veraison from
 field-grown vines during stage III of berry growth at 89
 days after full bloom. Berries soluble solid concentration
 ranged between 18-19 brix. Sampled vines were located at
 the University of California, Davis, Experimental
 Vineyard. cDNAs were made by oligo-dT priming and direct
 onally cloned. 5' and 3' adaptors were used in cloning as
 follows: 5'-AAGCAGGATCAACAGAGTGGCCATTCGCGCGG-3' and
 5'-ATTCTAGAGCGGAGGCGCGGATG-dt(30)NN-3'. Library was
 constructed using the Clontech Creator SMART kit and
 size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Alignment Scores:
 Pred. No.: 1.69e-108 Length: 760
 Score: 1094.00 Matches: 195
 Percent Similarity: 93.30% Conservative: 14
 Best Local Similarity: 87.05% Mismatches: 15
 Query Match: 77.98% Indels: 0
 DB: 6 Gaps: 0

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US-10-660-499A-2 (1-255) x CB981222 (1-760)
QY 32 AlaHisAlaThrPheTyrGlyGlySerAspAlaSerGlyThrMetGlyValAlaCysGly 51
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DB 2 GCTCAGGCTACGTTTATGAGGCAATGATGCTCTGGGACATGCGACAGTCTTGGA 61
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 52 TyrGlyAsnLeuTyrAlaThrArgIlyTyrArgThrAlaAlaLeuSerThrAlaLeu 71
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 62 TATGAAACCTTGAATCTACTGATATGGAACAAGACGCACTTTGAGCACAGCATTTG 121
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 72 PheAsnAspGlyValaSerCysGlyGlnCysTyrLysIleIleCysAspTyrLysSerAsp 91
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 122 TTCATATGATGAGGCTTCATGTGGCAATGCTTACAAAGTCAATATGATTAACAATTCGAT 181
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 92 SerArgTTPCysIleLysGlyArgSerValThrValThrAlaThrAsnPheCysProPro 111
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 182 TCACAGGAGGCAAGAAAGAGCTTCTATACCACTACCTGCAACAACTTTGCTCTCCA 241
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 112 AsnPheAlaLeuProAsnAsnAsnGlyTyrTTPCysAsnProProLeuLysHisPheAsp 131
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 242 AACTATGCTCTTCCAGCAACATGAGGGGTGTGCAACCCACCTGCGACATTTGAT 301
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 132 MetAlaGlnProAlaTTPGlyLysIleGlyIleTyrArgGlyGlyIleValProValLeu 151
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 302 ATGCTCAGCGCACATGGAAGAAAGATCGGATTAATTAAGAGGCGGATGCTCCAGTGTG 361
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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TITLE Generation of ESTs from *Aquilegia*
JOURNAL Unpublished (2005)
COMMENT Other ESTs: EST1130824
 Contact: Scott Hodges
 Department of Ecology, Evolution and Marine Biology
 University of California, Santa Barbara
 Santa Barbara, CA 93106, USA
 Tel: 805 893 7813
 Fax: 805 893 4724
 Email: hodges@lifesci.ucsb.edu
FEATURES Seq primer: M13 Reverse.
 Location/Qualifiers
 1..798
 /organism="Aquilegia formosa x Aquilegia pubescens"
 /mol_type="mRNA"
 /db_xref="taxon:338618"
 /clone="COLPS47"
 /tissue_type="mixed shoot and floral apical meristems, flower buds, leaves and roots"
 /lab_host="DH10B T1 (T1 and T5 phage resistance)"
 /note="Vector: PCMV SPORT6.1; Site 1: EcoRI; Site 2: NotI; F2, F3, and F4 lines of Aquilegia formosa x A. pubescens were grown from seed in greenhouses at UC Santa Barbara. From these plants three sets of tissue were collected: 1) Small flower buds (<10 mm) and very young inflorescences (71 & 29% by weight respectively), 2) Medium (7-20 mm) and large (at or near anthesis) flower buds (65 & 35% by weight respectively) and 3) Shoot apical meristems. A fourth set of tissue was collected from plants of A. formosa. These plants were grown from seed in sand and at approximately 1 month root tissue and leaf tissue of various developmental stages were collected (84 & 16% by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions: 1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled total RNA, mRNA was extracted and enriched for full-length messages and then normalized with proprietary methods by Invitrogen."

ORIGIN

Alignment Scores:
 Pred. No.: 4.02e-109 Length: 798
 Score: 1100.00 Matches: 196
 Percent Similarity: 92.64% Conservative: 18
 Best Local Similarity: 84.85% Mismatches: 17
 Query Match: 78.40% Indels: 0
 DB: 8 Gaps: 0

US-10-660-499a-2 (1-255) x DR939286 (1-798)

QY 3 lyeIlMeUleuValleuGlSerleuIlleGlYleuCyScpPhethrIleThrTyr 22
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 DB 104 AAGATTAATTTTGGCATTTGGTTGATGATTAATGATTAAGCTTAAGCTTAATTTGGAT 163
 QY 23 AlaPheSerProSerGlyTTPThrAsnAlaHisAlaThrPheTyrGlyGlySerAspAla 42
 164 GCTTTTCTCTCTGTTGGACAAAGCCCATGCTCTTTATGTTGTTGATGATGCT 223
 QY 43 SerGlyThrMetGlyGlyAlaCyGlyTyrGlyAsnLeuTyrAlaThrGlyTyrGlyThr 62
 224 TCAGGAACAATGGGGGAGCTTGGGTATGATTAATTAATCACTGATATGGGACT 283
 QY 63 ArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCyGlyGlnCysTyr 82
 DB 284 AGAACAGCAGCATTAAGTACTGCTCTGTTCAATGATGGGGCTCTTGTGGAACAATGGCTTC 343
 QY 83 lyeIllellecYsaApTyrLysSerAspSerArgTTPCysIleLeuGlyAARGSerValThr 102
 DB 344 AAGATCATATGTGATTCGAAGCAGATTCAAGATGGTGTGAAAGGAAGGTCTGTGACA 403
 QY 103 ValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAnglyGlyTyr 122
 |||||:::|||||

DB 404 GTCACTGCTACCAACTTCTGTCCACTTAATTGGCTCAAGCTAATGATATGAGGCTGG 463
 QY 123 CyAsnProFoleuLysHisPheAspMetAlaGlnProAlaTTPGlyTylleGlyTle 142
 DB 464 TGCATTCACACTCAAGCACTTGTATATGGCTCAGCTGCGTGGAGAAATTTGGTATTT 523
 QY 143 TyrArgGlyGlyLysLeuValProValLeuPheGlnArgValProCysLysLysHisGlyGly 162
 DB 524 TACAGAGGCGGAGATTTGCTGTGATCTACCAAGGGGTGCAATGAAGAACATGGTGA 583
 QY 163 ValArgPheSerValAsnGlyArgAspTyrPheGlyLeuValLeuIleSerAsnValGly 182
 DB 584 GTAAAGTTCACTTAACGGAGGAGCACTTTGAGCTTATATGATTAATGTCGCA 643
 QY 183 GlyAlaGlySerIleGlnSerValPheIleLysGlySerLysThrGlyTTPMetAlaMet 202
 DB 644 GGAAGTGGCTCAATTCATCTGTCGAATTAAGGCTCTTAAACAGGTTGATGGCAATG 703
 QY 203 SerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTyrLeuAsnGlyGlnSerLeuSer 222
 DB 704 TCAGGAATTTGGGAGCACTTAATTTGGCAGTCTTAATCTTATCTCAATGGCAATCTTTC 763
 QY 223 PheArgValThrThrAspGlyGlyThrArg 233
 DB 764 TTCAGGTCCACACTCCATGAGAGACTCGT 796

RESULT 9
 BG592843 789 bp mRNA linear EST 07-MAR-2003
 BG592843
 LOCUS EST491521 cSTS Solanum tuberosum cDNA clone cSTS2F23 5' sequence,
 DEFINITION mRNA sequence.
 ACCESSION BG592843
 VERSION BG592843.1 GI:13610983
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 789)
 van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chieningo,A.,
 Bougri,O., Buell,C.R., Roming,C., Tanksley,S. and Baker,B.
 Generations of ESTs from sprouting potato eyes
 Unpublished (2000)
 CONTACT: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics
 Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: M13F-R.

FEATURES
 source
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 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultiivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTS2F23"
 /tissue_type="sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"
 /clone_lib="cSTS"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
 taken from tubers. The tubers were incubated at 26C in the
 dark for 2-3 weeks prior to sprouting. The eyes were
 frozen in liquid nitrogen immediately upon removal from
 tubers."

ORIGIN

Alignment Scores:
 Pred. No.: 1.08e-108 Length: 789

QY 183 GYALAGYSerilegInserValPheilelyGlySerlythrglyTrrpMetAlaMet 202
 DB 210 GGGGCTGGATCTATTCAATCAATCAATCAAGGCTCCCGGACAGTTCGATGGCCATG 151
 QY 203 SerArgAsnTrrpGlySerAntTrrpGlnSerAsnAlaTrrleuAnGlyGlnSerLeuSer 222
 DB 150 TCAGGAACCTGGGGAGCTAACTGGCAGTCTTAATGCTCATCTCAATGGCCAGTCTGTGCC 91
 QY 223 PheArgValThrThrThrArgGlyGlnThrArgValPheGlnAspIleValProValSer 242
 DB 90 TTCAGAGTACCAACCACTAGTAGAGTACCAGAAATGACAAATGTGTGTCTTCAGAT 31
 QY 243 TrrThrPheGlyGlnThrPheSerSer 251
 DB 30 TGGGGGTTGGTCAAGACCTTCTTACG 4
 RESULT 7
 CF208597 808 bp mRNA linear EST 01-AUG-2003
 LOCUS CAB20003_1YA_F04 Cabernet Sauvignon Flower bloom - CAB2 Vitis
 DEFINITION Vitis vinifera cDNA clone CAB20003_1YA_F04 5', mRNA sequence.
 ACCESSION CF208597
 VERSION CF208597.1 GI:33402970
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Rosids; Vitaceae; Vitis.
 1 (bases 1 to 808)
 REFERENCE
 AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
 Jones, K. and Cook, D.
 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
 berries at various developmental stages
 Unpublished (2003)
 COMMENT
 Contact: Douglas Cook, PhD
 CABES Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcocok@ucdavis.edu
 Seq primer: ACGGTACCGGACATATGCC.
 FEATURES
 source
 1..808
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB20003_1YA_F04"
 /sex="Hermaphrodite"
 /dev_stage="Bloom"
 /clone_1lb="Cabernet Sauvignon Flower bloom - CAB2"
 /note="Organ: Flower. Bloom. Vector: pDNR. Site: 1. SfiI;
 Site 2: SfiI. CAB2 is a cDNA library of Vitis vinifera cv.
 'Cabernet Sauvignon' Clone 8 berries. Samples were
 collected at full bloom (80 to 100% flowers showing
 dehiscence of calypters or caps and anthers fully
 extended). Sampled vines were located at the University of
 California, Davis, Experimental Vineyard. cDNAs were made
 by oligo-dT priming and directionally cloned. 5' and 3'
 adaptors were used in cloning as follows:
 5'-AACGAGGTATCAACGACAGAGTGGCCATTCAGCGCCGG-3' and
 5'-ATTCTAGAGCGCAGCGCCGACATG-AT(30)NM-3'. Library was
 constructed using the Clontech Creator SMART kit and
 size-selected to contain the 0.5-3 kb size fraction."

Query Match: 78.51% Indels: 1
 DB: 6 Gaps: 1
 US-10-660-499A-2 (1-255) x CF208597 (1-808)
 QY 1 MetGlyLysIleMetLeu--ValleuGlySerLeuIleGlyLeuGlyCysPheThrIle 19
 DB 84 ATGGCGAAAATCTGCTCATGCTTTAGCAATGGTCGGGTAAATTTGCTATTTTCTCG 143
 QY 20 ThrThrTrrAlaPheSerProSerGlyTrrThrAsnAlaHisAlaThrPheTrrGly 39
 DB 144 AATGTTAATGCCCTTATCTGCTTCGGGTGACTAAAGCTCAGCTACGTTTATGAGAGG 203
 QY 40 SerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTrrGlyAsnLeuTrrAlaThrGly 59
 DB 204 AGTGAATGCTCTTGGGACATGGAGGGCTTGTGATATGAAATCTTGAATCTACTGGA 263
 QY 60 TrrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGly 79
 DB 264 TATGGAAACAAGACGGCAGCTTTAGACACAGCATTTGTCAATGATGGGCTTCATGAGG 323
 QY 80 GlnCysTrrLysIleIleCysAspTrrLysSerAspSerArgTrrCysIleLysGlyArg 99
 DB 324 CAATGCTACAGATCATATGATGATTAACAATCCGATTCACAGTGTGCAAGAAAGAGCT 383
 QY 100 SerValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsn 119
 DB 384 TCTGTACCATCATCTGCACAAACTTTTCCCTCCAACTATGCTCTTCCAGCAACAT 443
 QY 120 GlyGlyTrrCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaTrrGlyLys 139
 DB 444 GAGGGGTGTGGCAACCCGCGACGATTCGATATGAGCTCAGCAGCATGGAGAAAG 503
 QY 140 IleGlyIleTrrArgGlyGlyIleValProValLeuPheGlnArgValProCysLysLys 159
 DB 504 ATCGGTATTTCACAGAGCGCGAGATCGCCACAGTCTGTTCAAAGGGTTCATGTAAGAG 563
 QY 160 HisGlyGlyValAlaPheSerValAsnGlyArgAspTrrPheGlnLeuValLeuIleSer 179
 DB 564 CATGGTGGTGTAGATCATGATGTTATGAAAGACTTCTTCGAATTAATGATTAAGAC 623
 QY 180 AsnValGlyGlyAlaGlySerilegInserValPheileGlySerlythrglyTrrp 199
 DB 624 AATGTAGCTGGGGCTGGATCTAATCAATCAATCAATCAAGGCTCCGAGCAGATGG 683
 QY 200 MetAlaMetSerArgAsnTrrpGlySerAntTrrpGlnSerAsnAlaTrrleuAnGlyGln 219
 DB 684 ATGGCCATGTCCGAGAACTGGGAGCTAACTGGCAGTCTTAATGCCATTCGAATGGCCAG 743
 QY 220 SerLeuSerPheArgValThrThrTrpAspGlyGlnThrArgValPheGlnAspIleVal 239
 DB 744 TCTCTGTCTTCAAGGTCAACCACTGATGAGTAGACCATCAATTCGACATGTTGTG 803
 QY 240 Pro 240
 DB 804 CCT 806
 RESULT 8
 DR939286 798 bp mRNA linear EST 02-AUG-2005
 LOCUS EST1130825 Aquilegia cDNA library Aquilegia formosa x Aquilegia
 DEFINITION pubescens cDNA clone COLPS47, mRNA sequence.
 ACCESSION DR939286
 VERSION DR939286.1 GI:71708649
 KEYWORDS EST.
 SOURCE Aquilegia formosa x Aquilegia pubescens
 ORGANISM Aquilegia formosa x Aquilegia pubescens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 Ranunculaceae; Aquilegia.
 1 (bases 1 to 798)
 REFERENCE
 AUTHORS Hodges, S.A., Rensink, W., Buehl, C.R., Borevitz, J., Kramer, E.,
 Nordborg, M. and Tomkins, J.

Pred. No.: 8,39e-113 Length: 701
 Score: 1133.00 Matches: 201
 Percent Similarity: 93.89% Conservative: 14
 Best Local Similarity: 87.77% Mismatches: 14
 Query Match: 80.76% Indels: 0
 DB: 8 Gaps: 0

US-10-660-499a-2 (1-255) x CX018002 (1-701)

QY 23 AAlpHeSePrSeSerGlyTTPThRaMaLaHleAlaThPheThyGlyGlySerAaPaLa 42
 DB 690 GCCTTACGCTCTTGCGGTGAATAAGCTCAAGCTTATGAGGGGCACTGATGCC 631
 QY 43 SerGlyThMeGlyGlyAlaCyGlyTYTGlyAsnLeuTYAlaThrglyTYGlyThr 62
 DB 630 TCTGGGACTATGGAGGGGCTTGATATGAACTTGATCTCACTGGATATGAGCA 571
 QY 63 ArgThAlaAlaLeuSerThRaLaLeuPheAsnAspGlyAlaSerCysGlyGlyGly 82
 DB 570 AGAACGGCAGCTTTGAGCAGCATTTGTCATATGAGGGCTTCATGTGGCAATGCTAC 511
 QY 83 LysIleIleCysAspTYrIysSerAspSerArgTTPCysIleIysGlyArgSerValThr 102
 DB 510 AAGATCATATGTGATTTACCAAGTCGATTCACAGTGGTGAAGAAAGAGCTTCTGTGACC 451
 QY 103 ValThAlaThAsnPheCysPProAsnPhaAlaLeuProAsnAsnAnglyGlyTTP 122
 DB 450 ATCACTGCAACAACTTTGGCTCCCAACTATGCTCTTCCAAAGCAACATGAGGGGTGG 391
 QY 123 CysAsnProLeuIysHsIspheAspMetAlaGlaProAlaTTPGluIysIleGly 142
 DB 390 TGCACCCACCCCTTGACGATTCGATATGCTCAGCAGCAGCAAGGAAAGATCGGATTT 331
 QY 143 TYrArgGlyGlyIleValProValIleuPheGlnArgValProCysIysIysHsIleGly 162
 DB 330 TACAGAGGGGGATTCCTCCAGTGTCTTCCAAAGGTTCCATGAAGAGCATGGGTGT 271
 QY 163 ValArgPheSerValAsnGlyArgAspTYrPheGluLeuValIleIleSerAsnValGly 182
 DB 270 GTTAGATTCAAGTGTATATGAGAGACTACTCGAATTAGTATTAAGCAATGTAGCT 211
 QY 183 GlyAlaGlySerIleGlnSerValIleIleIysGlySerIysThrglyTTPMetAlaMet 202
 DB 210 GGGGCTGAGATCTATTCATCAATCAATCAATCAAGGCTCCGAGCAGGTGGATGGCCATG 151
 QY 203 SerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTYrIleuAsnGlyGlnSerLeuSer 222
 DB 150 TCCAGAACTGGGAGACTAATGCGAGTCTAATGCTTCAATGGCCAGTCTCTGTC 91
 QY 223 PheArgValThrTh 242
 DB 90 TTCAGAGTCAACCACTGATGAGTGACCCAGAAATGTCACATGTGTGCTTCAGAT 31
 QY 243 TTPThPheGlyGlnThPheSerSer 251
 DB 30 TGGGGGTTGTGTCAGACTTCTCTAGC 4

RESULT 6
 CX018002/ 733 bp mRNA linear EST 07-DEC-2004
 LOCUS EST 1711 wild type Ugni blanc SSH library Vitis vinifera cDNA clone
 DEFINITION 3596 UB_S9_F11, mRNA sequence.
 ACCESSION CX018002
 VERSION CX018002.1 GI:56409750
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 733)
 REFERENCE
 AUTHORS Fernandez, L., Romeu, C., Grimpel, J., Torregrosa, L. and Ageorges, A.
 TITLE Functional Genomics of Fruit Early Development in Grape (Vitis

JOURNAL vinifera)
 COMMENT Unpublished (2004)
 Contact: Ageorges A.
 Unite de Recherche des Produits de la Vigne
 Institut National de la Recherche Agronomique
 2, place Viala, 34 060 Montpellier Cedex 01, France
 Tel: 00-33-(0)4-99-61-27-56
 Fax: 00-33-(0)4-99-61-28-57
 Email: ageorges@enscm.inra.fr
 Seq primer: 17.
 Location/Qualifiers
 1..733
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Ugni Blanc"
 /db_xref="taxon:29760"
 /clone="3596 UB_S9_F11"
 /dev_stage="Green stage"
 /lab_host="DH5 alpha"
 /clone_lib="Wild type Ugni blanc SSH library"
 /note="Organ: Fruit; Vector: pGem-T; Total RNA was isolated from 3, 6 and 15 days post anthesis for wild type and 'fleshless' mutated berries. cDNA was prepared from RNA (equal amount of the three developmental stages for each genotype) using the smart PCR cDNA system (Clontech). cDNA library was performed with the PCR-select cDNA subtraction kit (BD Biosciences, Clontech) using RNA from wild type as the tester and RNA from mutant as the driver."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 8,94e-113 Length: 733
 Score: 1133.00 Matches: 201
 Percent Similarity: 93.89% Conservative: 14
 Best Local Similarity: 87.77% Mismatches: 14
 Query Match: 80.76% Indels: 0
 DB: 8 Gaps: 0

US-10-660-499a-2 (1-255) x CX018002 (1-733)

QY 23 AAlpHeSePrSeSerGlyTTPThRaMaLaHleAlaThPheThyGlyGlySerAaPaLa 42
 DB 690 GCCTTACGCTCTTGCGGTGAATAAGCTCAAGCTTATGAGGGGCACTGATGCC 631
 QY 43 SerGlyThMeGlyGlyAlaCyGlyTYTGlyAsnLeuTYAlaThrglyTYGlyThr 62
 DB 630 TCTGGGACTATGGAGGGGCTTGATATGAACTTGTATCTCACTGGATATGAGCA 571
 QY 63 ArgThAlaAlaLeuSerThRaLaLeuPheAsnAspGlyAlaSerCysGlyGlyGly 82
 DB 570 AGAACGGCAGCTTTGAGCAGCATTTGTCATATGAGGGCTTCATGTGGCAATGCTAC 511
 QY 83 LysIleIleCysAspTYrIysSerAspSerArgTTPCysIleIysGlyArgSerValThr 102
 DB 510 AAGATCATATGTGATTTACCAAGTCGATTCACAGTGGTGAAGAAAGAGCTTCTGTGACC 451
 QY 103 ValThAlaThAsnPheCysPProAsnPhaAlaLeuProAsnAsnAnglyGlyTTP 122
 DB 450 ATCACTGCAACAACTTTGGCTCCCAACTATGCTTCCAGCAACATGAGGGTGG 391
 QY 123 CysAsnProLeuIysHsIspheAspMetAlaGlnProAlaTTPGluIysIleGly 142
 DB 390 TGCACCCACCCCTTGACGATTTGATATGCTCAGCAGCAGCATGGGAAAGATCGGATTT 331
 QY 143 TYrArgGlyGlyIleValProValIleuPheGlnArgValProCysIysIysHsIleGly 162
 DB 330 TACAGAGGGGGATTCCTCCAGTGTCTTCCAAAGGTTCCATGTGAAGAGCATGGGTGT 271
 QY 163 ValArgPheSerValAsnGlyArgAspTYrPheGluLeuValIleIleSerAsnValGly 182
 DB 270 GTTAGATTCAAGTGTATATGAGAGACTTCTCGAATTAGTATTAAGCAATGTAGCT 211

QY 101 ValThValThAlaThraPheCysProProAsnPheAlaLeuProAsnAsnGly 120
 Db 392 GTGACCATTAACACCAACAACTTTGCTCTTAACCTTCTCCCAACAAATGCCGGA 451
 QY 121 GATTCGAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPGluLysIle 140
 Db 452 GGCTGGGACATCAACCCCTCCAGCACTTGACATGGCTGCTGCTGGAAGAATC 511
 QY 141 GATTCGAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPGluLysIle 160
 Db 512 GGTATCTACAGAGCGGAAATTTGCGCTTTGTTCCAAAGGTTCTTCCAGAGCAT 571
 QY 161 GATTCGAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPGluLysIle 180
 Db 572 GGTGAGAGTGGTTCAAGATCAATGAGAGACATATTTCAGCTGTTATGATTAAGCAT 631
 QY 181 ValGlyValAlaGlySerIleGlnSerValPheIleLysSerIleLysSerIle 200
 Db 632 GTTGGGCGGACGATCTATCCAGTCTGTCATCAAGGATCCAAACCTGGGTGATG 691
 QY 201 AlaMetSerArgAsnTPGlySerAsnTPGlySerAsnAlaTyrLeuAsnGlyGlnSer 220
 Db 692 GCATGTCAAGAGACTGGGAGCTAAGCTGCAATCCAGCTTATCTCATGGCCATCA 751
 QY 221 LeuSerPheArgValTh 240
 Db 752 TTTCGCTTCAGGGTCAACCACTAGATGTGTGACTGACCAATTCCTGACATGTGCT 811

RESULT 3 746 bp mRNA linear EST 11-APR-2001
 LOCUS BG585324
 DEFINITION EST487068 MHAM Medicago truncatula/Gloms versiforme mixed EST
 library cDNA clone pMHAM-22F13 5' end, mRNA sequence.

ACCESSION BG585324 GI:13600388
 VERSION BG585324.1
 KEYWORDS Medicago truncatula/Gloms versiforme mixed EST library
 SOURCE Medicago truncatula/Gloms versiforme mixed EST library
 ORGANISM Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 746) Town, C.D., Van Aken, S., Utterback, T., Cho, J.
 AUTHORS Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J.
 TITLE ESTs from roots of Medicago truncatula after colonization with
 Gloms versiforme, 2001
 JOURNAL Unpublished (2001)
 COMMENT Contact: Harrison M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Noble EST name: N380798e TIGR sequence name: MTDC031TK More
 information is available at: http://www.medicago.org
 Seg primer: Skmod (CTA GAA CTA gtc gat CC).
 Location/Qualifiers

FEATURES
 source 1..746
 /organism="Medicago truncatula/Gloms versiforme mixed EST
 library"
 /mol_type="mRNA"
 /cultivar="Medicago truncatula genotype A17"
 /db_xref="taxon:119092"
 /clone="pMHAM-22F13"
 /tissue_type="roots colonized with Gloms versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
 post-inoculation with Gloms versiforme. The library was
 made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0R"
 /clone_1ib="MHAM"
 /note="Vector: pBluescript SK-. Site 1: EcoRI, Site 2:
 XhoI, cDNA was prepared from polyA+ enriched RNA from
 roots harvested at 10, 17, 22, 31 and 38 days

post-inoculation with Gloms versiforme. The cDNA was
 directionally ligated into the UniZap XR vector from
 StrataGene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-cap phage using Ex-aseII
 helper phage and propagated in XL0R cells."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,656-114 Length: 746
 Score: 1149.00 Matches: 205
 Percent Similarity: 93.56% Conservative: 13
 Best Local Similarity: 87.98% Mismatches: 14
 Query Match: 81.90% Indels: 1
 DB: 2 Gaps: 0

US-10-660-499a-2 (1-255) x BG585324 (1-746)

QY 24 PheSerProSerGlyTTPThraAlaHisAlaThraPheTyrGlySerAspAlaSer 43
 Db 2 TTCAAAGCTTCGATGAGACCAATGCTCATGCAACTTTTATGCGGTAGTGGCGAA 61
 QY 44 GATTCGAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPGluLysIle 63
 Db 62 GGCATATGGAGAGACTTGTGTATGGAACTGTATTCACAAAGGATGGGACAGA 121
 QY 64 ThraAlaLeuSerThraAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrLys 83
 Db 122 ACAGCTGATTAAGTACTGCTTTGTTTATGATGAGAGCTTCATGTGGCAATCTCAAA 181
 QY 84 IleIleCysAspTyrLysSerAspSerArgTTPCysIleLysGlyArgSerValThThVal 103
 Db 182 ATCATTTGATGATTAAGACAGACCCCAAGTGTGATTAAGAGAGATCTATTACCAT 241
 QY 104 ThraAlaThraPheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTTPCys 123
 Db 242 ACAGCCCAAAATTCGCTCTCCAAATTTGATCTTCACACACCATGAGGTTGGTC 301
 QY 124 AsnProProLeuLysHisPheAspMetAlaGlnProAlaTPGluLysIleTyr 143
 Db 302 AACCCACTCTTAAGCATTTTGTATGGACCAACCTGCTGGAAAGATTGGAATCTAT 361
 QY 144 ArgGlyGlyTleValProValLeuPheGlnArgValProCysLysLysGlyGlyVal 163
 Db 362 AGAGAGGAGATCTCTCTCTTATTTCAAGGGTCTTGGCAAAAGCATYGAGAGATT 421
 QY 164 ArgPheSerValAsnGlyArgAspTyrPheGluLeuValLeuIleSerAsnValGlyLys 183
 Db 422 AGGTTCAGTGTGATGAGAGAGCTTGTAGTGTGATGTGATGACCAATCTGGCTGAT 481
 QY 184 AlaGlySerIleGlnSerValPheIleLysGlySerIleThraGlyTTPMetAlaMetSer 203
 Db 482 GCTGCTCAATCCAACTGTTTCCATTAAGTTTCCAAACATGATGGAGGCTATGTCA 541
 QY 204 ArgAsnTPGlySerAsnTPGlySerAsnAlaTyrLeuAsnGlyGlnSerIleSerPhe 223
 Db 542 AGAATTTGGGTCAAATGGCAATCCAAATGCTTATTTGAATGATGATGATGATGCTTC 601
 QY 224 ArgValTh 243
 Db 602 AAGTTCACCAATCCATGAGAGATGACCAAGAACTTTCCAGACATGTTCTTCCAAATGG 661
 QY 244 -ThraPheGlyGlnThraPheSerSerProValGlnPhe 255
 Db 662 GGAATTTGGTCAATCTTCTCTAGCAAGATCCAGTTC 698

RESULT 4 745 bp mRNA linear EST 07-DEC-2004
 LOCUS CX017854/C
 DEFINITION EST 1563 wild type Ugni blanc SSH library vltis vinifera cDNA clone
 3596 UB_86_H01, mRNA sequence.
 ACCESSION CX017854
 VERSION CX017854.1 GI:56409602

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2006, 21:11:45 ; Search time 3822 Seconds
(without alignments)
3121.587 Million cell updates/sec

Title: US-10-660-499a-2
Perfect score: 1403
Sequence: 1 MGKIMLVGSLIGLCFFIT.....QDIVPVSMTFGTFFSPVGF 255

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354128 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model -DEV=xlp
-Q/cg2.1/USPTO.spool.p/US10660499/runat.10012006.105621.16436/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10660499.@CGN_1_1.8010.@runat.10012006.105621.16436 -NCPU=6 -ICPU=3
-NO NMAP -LARGEDUTERY -NEG SCORES=30 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1170	82.4	818	7	COL132031	COL132031 GR_EB44K
2	1150	83.0	813	7	COL100655	COL100655 GR_EB002
3	1149	81.9	746	2	BG585324	BG585324 ESTT487088
4	1134	80.8	745	8	CX017425	CX017425 EST 1563
5	1133	80.8	701	8	CX017425	CX017425 EST 1134
6	1133	80.8	733	8	CX018002	CX018002 EST 1711
7	1101.5	78.5	808	6	CF208597	CF208597 CAB20003

8	1100	78.4	798	8	DR39286	EST113082
9	1096	78.1	789	2	BG592843	EST491521
10	1094	78.0	760	6	CB981222	CAB70004
11	1094	78.0	832	8	CX187525	96-E02272
12	1089	77.6	617	2	BE607657	8615c07.Y
13	1084	77.3	790	5	BQ505051	EST612466
14	1082.5	77.2	779	6	CF208603	CAB20003
15	1081.5	77.1	777	6	CF208603	CAB20003
16	1077	76.8	725	2	BG643838	EST512032
17	1071	76.3	764	2	BG592929	EST491607
18	1064	75.8	895	7	CK288799	EST751521
19	1064	75.8	918	7	CK286920	EST749642
20	1064	75.8	936	7	CK288970	EST751692
21	1064	75.8	952	7	CK291076	EST753790
22	1059.5	75.5	775	6	CF208600	CAB20003
23	1048.5	74.7	754	6	CF208598	CAB20003
24	1040.5	74.2	721	2	BQ126936	EST742582
25	1039	74.1	786	10	CL981726	OBIFSC046
26	1037	73.9	806	4	CNS0ACQO	BX818225 Arabidops
27	1034.5	73.7	705	6	CF443494	EST679839
28	1033.5	73.7	768	8	CX017719	EST 1428
29	1030	73.4	630	6	CB915761	VD0102G01
30	1030	73.4	632	6	CB919381	VD046F01
31	1030	73.4	686	2	BG598019	EST496697
32	1027	73.2	768	7	CV497500	61708.1 M
33	1021	72.8	735	6	CF208736	CAB20003
34	1020.5	72.7	765	6	CF208736	CAB20003
35	1019	72.6	811	7	CO101426	GR_EB002
36	1012	72.1	663	2	BI207194	EST525234
37	1012	72.1	759	1	AJ794895	AJ794895
38	1009	71.9	686	7	CN782073	EST00168
39	1007	71.8	613	6	CB919975	VVD057G05
40	1006	71.7	673	1	AJ560126	AJ560126
41	1005	71.6	737	8	DR912239	EST110377
42	1003	71.5	610	6	CB919142	VD041G12
43	1001	71.3	851	6	CF636608	zmtw00.0
44	993.5	70.8	660	6	CB006556	VVC005B09
45	993	70.8	692	1	AI781569	EST262448

ALIGNMENTS

RESULT 1	COL132031	818 bp	mrna	linear	EST 17-JUN-2004
LOCUS	COL132031				
DEFINITION	GR_EB44K03.r GR_EB Gossypium raimondii cDNA clone GR_EB44K03 3',				
ACCESSION	COL132031				
VERSION	COL132031.1	GI:48881009			
KEYWORDS	EST.				
SOURCE	Gossypium raimondii				
ORGANISM	Gossypium raimondii				
REFERENCE	Bukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.				
AUTHORS	1 (bases 1 to 818)				
	Kim H., Yu Y., Kudrna D., Hatfield J., Stum D., Mueller C., Udall J., A., Rapp R.A., Wendel J.F., Rao K., Soderlund C. and Wing R.A.				
TITLE	Global assembly of Cotton ESTs				
JOURNAL	Unpublished (2004)				
COMMENT	Contract: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: twing@genome.arizona.edu Plate: 44 row: K column: 03.				
FEATURES	Location/Qualifiers				
source	1..818				
	/organism="Gossypium raimondii"				
	/mol_type="mrna"				

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QY 241 ValSerTrpThrPheGlyGlnThrPhe 249
Db 421 GCTGGTTGGCAATTCGGACAACTTTT 447

RESULT 15

US-08-298-829-6
; Sequence 6, Application US/08298829
; Patent No. 5620882
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,829
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/885,970
; FILING DATE: 18-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12

US-08-298-829-6

Alignment Scores:
Pred. No.: 3,79e-58 Length: 727
Score: 586.00 Matches: 100
Percent Similarity: 82.55% Conservative: 23
Best Local Similarity: 67.11% Mismatches: 26
Query Match: 41.77% Indels: 0
DB: 2 Gaps: 0

US-10-660-499A-2 (1-255) x US-08-298-829-6 (1-727)

QY 101 ValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 120
Db 1 ATAACCGTGACAGCCACCACTTTTGTCCACCTAATGCTTTATCTAGTGACATGGC 60
QY 121 GlyTrpCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaTrpGluLysIle 140
Db 61 GGGTGGTGCATTCCTCCCGCAGAACACTTTGATTTGGCCGAAACCGGCATCTTGGCGATA 120
QY 141 GlyIleTyArgGlyGlyIleValProValLeuPheGlnArgValProCysLysLysHis 160
Db 121 GCAGAAATATCGAGCTGGAAATCGTCTGTTATGTTTCAGAAAGGTGTCTATGTGAAGAAA 180
QY 161 GlyGlyValArgPheSerValAsnGlyArgAspTyrPheGluLeuValLeuIleSerAsn 180
Db 181 GGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATGGTGTGGATAACGAAC 240
QY 181 ValGlyGlyAlaGlySerIleGlnSerValPheIleLysGlySerLysThrGlyTrpMet 200
Db 241 GTGGAGGGGCGAGGGGATATAACGTCAAGGGTTCAGAAACAGGATGGCTA 300
QY 201 AlaMetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaTyrLeuAsnGlyGlnSer 220
Db 301 CCTATGTCAGAAATTTGGGCCAAAACTGGCAGAGCAATGCTTACCTTAACGACAAAGC 360
QY 221 LeuSerPheArgValThrThrAspGlyGluThrArgValPheGlnAspIleValPro 240
Db 361 CTCCTCTTTTAAAGTGACTGCCAGCGATGGCAGGACTATCACAGCCTTACAATGTAGTGCCT 420
QY 241 ValSerTrpThrPheGlyGlnThrPhe 249
Db 421 GCTGGTTGGCAATTCGGACAACTTTT 447

Search completed: January 12, 2006, 00:02:00
Job time : 190 secs


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/ ORIGINAL SOURCE:
/ ORGANISM: Gossypium hirsutum
/ STRAIN: Coker 312
/ DEVELOPMENTAL STAGE: 10 day old fiber cells
/ TISSUE TYPE: fiber cells
/ IMMEDIATE SOURCE:
/ LIBRARY: CKEB10
/ CLONE: B12
US-08-298-687A-6

Alignment Scores:
Pred. No.: 3,796-58 Length: 727
Score: 586.00 Matches: 100
Percent Similarity: 82.55% Conservative: 23
Best Local Similarity: 67.11% Mismatches: 26
Query Match: 41.77% Indels: 0
DB: 2 Gaps: 0

US-10-660-499A-2 (1-255) x US-08-298-687A-6 (1-727)
QY 101 ValThrValThrAlaThrAsnPhcysProProAsnPhaAlaLeuProAsnAsnAngly 120
DB 1 ATAAACCGTACAGCCCACTTTGTCCACTATGCTTATCTAGTACATGAC 60
QY 121 GlyTTPCyAsnProProLeuYshIsPhaAspMetAlaGlnProAlaTTPGluYsile 140
DB 61 GGGTGTGCATTCCTCCCAAGACACCTTTGATTTGGCCGACCGCATTCCTGGGATA 120
QY 141 GlyIleTyArgGlyIleValProValLeuPhaGlnArgValProCysIlyshIs 160
DB 121 GCAGATATCGAGCTGAGATTCGCTGTTATGTTACAGAGGCTGCATGTGAGAGAA 180
QY 161 GlyIleValArgPheserValAnglyArgAspTyrPhaGlnLeuValLeuIleserAn 180
DB 181 GAGGCGATCAGGACCACTGATGATGACATTCCTACTTCAACATGCTTATGATACGAAC 240
QY 181 ValGlyValAlaGlySerIleGlnSerValPheIleYsGlySerIlyThrGlyTpmet 200
DB 241 GTGGAGGGGCGAGGATTTACGTACATGCTCATCAAGGTTCCAGAACAGATGGCTA 300
QY 201 AlaMetSerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTyrLeuAsnGlyGlnSer 220
DB 301 CCTATGTCAGAAATTTGGGGCCAAACCTGGCAGAGCAATGCTTAACTTAAACGACAAAC 360
QY 221 LeuSerPheArgValThrThrThraAspGlyIleThraArgValPheGlnAspIleValPro 240
DB 361 CTCTCTTTTAAAGTACCTGCCAGCATGCGACGACATATCAACAGCTTACATATGAGCT 420
QY 241 ValSerTTPThrPheGlyGlnThraPhe 249
DB 421 GCTGCTTGGCAATTCGAGCAAACTTTT 447

RESULT 14
US-08-530-797-5
/ Sequence 5, Application US/08530797
/ Patent No. 5597718
/ GENERAL INFORMATION:
/ APPLICANT: John, Maliyakal E.
/ APPLICANT: Umbeck, Paul F.
/ APPLICANT: Brill, Winston J.
/ TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
/ TITLE OF INVENTION: FOR ALTERED FIBER
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles and Brady
/ STREET: P.O BOX 2113
/ CITY: MADISON
/ STATE: WISCONSIN
/ COUNTRY: U.S.A.
/ ZIP: 53701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage

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/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh
/ SOFTWARE: Microsoft Word 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/530,797
/ FILING DATE: 20-SEP-1995
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/617,239
/ FILING DATE: 21-NOV-90
/ APPLICATION NUMBER: US 07/253,243
/ FILING DATE: 04-OCT-88
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nicholas J. Seay
/ REGISTRATION NUMBER: 27,386
/ REFERENCE/DOCKET NUMBER: 1122990245
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 727 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ ANTI-SENSE: no
/ HYPOTHEICAL: no
/ ORIGINAL SOURCE:
/ ORGANISM: Gossypium hirsutum
/ STRAIN: Coker 312
/ DEVELOPMENTAL STAGE: 10 day old fiber cells
/ TISSUE TYPE: fiber cells
/ IMMEDIATE SOURCE:
/ LIBRARY: CKEB10
/ CLONE: B12
US-08-530-797-5

Alignment Scores:
Pred. No.: 3,796-58 Length: 727
Score: 586.00 Matches: 100
Percent Similarity: 82.55% Conservative: 23
Best Local Similarity: 67.11% Mismatches: 26
Query Match: 41.77% Indels: 0
DB: 2 Gaps: 0

US-10-660-499A-2 (1-255) x US-08-530-797-5 (1-727)
QY 101 ValThrValThrAlaThrAsnPhcysProProAsnPhaAlaLeuProAsnAsnAngly 120
DB 1 ATAAACCGTACAGCCCACTTTGTCCACTATGCTTATCTAGTACATGAC 60
QY 121 GlyTTPCyAsnProProLeuYshIsPhaAspMetAlaGlnProAlaTTPGluYsile 140
DB 61 GGGTGTGCATTCCTCCCAAGACACCTTTGATTTGGCCGACCGCATTCCTGGGATA 120
QY 141 GlyIleTyArgGlyIleValProValLeuPhaGlnArgValProCysIlyshIs 160
DB 121 GCAGATATCGAGCTGAGATTCGCTGTTATGTTACAGAGGCTGCATGTGAGAGAA 180
QY 161 GlyIleValArgPheserValAnglyArgAspTyrPhaGlnLeuValLeuIleserAn 180
DB 181 GAGGCGATCAGGACCACTGATGATGACATTCCTACTTCAACATGCTTATGATACGAAC 240
QY 181 ValGlyValAlaGlySerIleGlnSerValPheIleYsGlySerIlyThrGlyTpmet 200
DB 241 GTGGAGGGGCGAGGATTTACGTACATGCTCATCAAGGTTCCAGAACAGATGGCTA 300
QY 201 AlaMetSerArgAsnTTPGlySerAsnTTPGlnSerAsnAlaTyrLeuAsnGlyGlnSer 220
DB 301 CCTATGTCAGAAATTTGGGGCCAAACCTGGCAGAGCAATGCTTAACTTAAACGACAAAC 360
QY 221 LeuSerPheArgValThrThrThraAspGlyIleThraArgValPheGlnAspIleValPro 240
DB 361 CTCTCTTTTAAAGTACCTGCCAGCATGCGACGACATATCAACAGCTTACATATGAGCT 420

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DB      475 AGCCGAATTGGGGTCAAAACTGGCAG 501
RESULT 12
US-07-885-970A-6
; Sequence 6, Application US/07885970A
; Patent No. 5495070
; GENERAL INFORMATION:
; APPLICANT: John, Maljykal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,970A
; FILING DATE: 19920518
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKBIO
; CLONE: B12
; US-07-885-970A-6

Alignment Scores:
Pred. No.:      3,796-58      Length:      727
Score:          586.00      Matches:      100
Percent Similarity: 82.55%      Conservative: 23
Best Local Similarity: 67.11%      Mismatches:  26
Query Match:     41.77%      Indels:       0
DB:              Gaps:       0

US-10-660-499A-2 (1-255) x US-07-885-970A-6 (1-727)
QY      101 ValTrvraTThraAlaThrAsnPhcCySProProAsnPhaAlaLeuProAsnAaAengLy 120
      ::::::::::::::::::::
DB      1 ATAAcCGTGAcGcCACCACtTTGTTCcACCTAaTAcCTTATCTaTGAcAATGcC 60
QY      121 GtYTpCyAsnProDroLeuYshIsPheAsPMetAlaGInDroAlaATpGtUlySeIle 140

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[illegible]

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-Apr-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..501
OTHER INFORMATION: /product= "strawberry FaEx1"
US-08-845-539-3

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Alignment Scores:
Pred. No.: 3,75e-62 Length: 501
Score: 618.50 Matches: 110
Percent Similarity: 75.74% Conservative: 18
Best Local Similarity: 65.09% Mismatches: 38
Query Match: 44.08% Indels: 3
DB: Gaps: 2

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US-10-660-499a-2 (1-255) x US-08-845-539-3 (1-501)
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DB 1 GGAACCATGGGGGGGCTGTGTGATATGAAACCTTACAGCCAGGCTACGAGATCAAC 60
QY 64 ThAlAlaLeuSerThAlaLeuPheAsnAspG1yAlaSerCySg1yG1nCyTYrTYLys 83
DB 61 ACTGCTGCGGTGAGCAAGCGCTGTCTTCAACAATGGCTGAGCGCGCTTGCTTCGAG 120
QY 84 l1e1leCyAspTYrLysSerAspSerArgTTPCyS1leYsg1yArg--SerValThr 102
DB 121 ATCAAGTGGCGC-----GACGACCCCAAGGTGGTGCACTCCGGAAGCCCTTCATTTC 174
QY 103 ValThAlaThraNpheCySPProAnPheAlaLeuProAnbAnbAnsg1yG1yTP 122
DB 175 GTACCGCCCAACCACTTGTCCCTCCCACTGCTGAGCCGACGACAAATGGGGTTGG 234
QY 123 CyAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPG1uLys1leG1y1le 142
DB 235 TGCACCTCTCCCGAGCCACTTGAGCTTCCGATGCCATGTTCTCAAGATCGCCGAG 294
QY 143 TYrArg1yG1y1leValProValLeuPheGlnArgValProCyS1yS1yS1yS1yG1y1y 162
DB 295 TACAAAGCCGGAATCGTCCCGCTCTTACCGCGCGGTCCATGCGTAAAGAAAGGGTGG 354
QY 163 ValArgPheSerValaAng1yArgAspTYrPheG1uLeuValLeu1leSerAnValG1y 182
DB 355 ATCAGGTTTCACATCAACGCGCCACAGTACTTCAACTGCTTGTGATCACCAAGTGGC 414
QY 183 G1yAlaG1ySer1leG1nSerValPhe1leYsg1ySer1yThrG1yTPMetAlaMet 202
DB 415 GGGCAGGGGATATCGTGAAGGTGAGGTGAAGGACCAACCGGGTGGATGCCAATG 474

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QY 203 SerArgAsnTPG1ySerAsnTPG1n 211
DB 475 AGCCGAATTTGGGGTCAAAACTGGCAG 501
RESULT 11
US-09-362-642-3
Sequence 3, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 501
TYPE: DNA
ORGANISM: Fragaria x ananassa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(501)
OTHER INFORMATION: strawberry expansin (FaEx1) partial cDNA clone
US-09-362-642-3

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Alignment Scores:
Pred. No.: 3,75e-62 Length: 501
Score: 618.50 Matches: 110
Percent Similarity: 75.74% Conservative: 18
Best Local Similarity: 65.09% Mismatches: 38
Query Match: 44.08% Indels: 3
DB: Gaps: 2

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US-10-660-499a-2 (1-255) x US-09-362-642-3 (1-501)
QY 44 G1YThMeG1yG1yAlaCySg1yTYrG1yAsnLeuTYrAlaThrG1yTYrG1yThrArg 63
DB 1 GGAACCATGGGGGGGCTGTGTGATATGAAACCTTACAGCCAGGCTACGAGATCAAC 60
QY 64 ThAlAlaLeuSerThAlaLeuPheAsnAspG1yAlaSerCySg1yG1nCyTYrTYLys 83
DB 61 ACTGCTGCGGTGAGCAAGCGCTGTCTTCAACAATGGCTGAGCGCGCTTGCTTCGAG 120
QY 84 l1e1leCyAspTYrLysSerAspSerArgTTPCyS1leYsg1yArg--SerValThr 102
DB 121 ATCAAGTGGCGC-----GACGACCCCAAGGTGGTGCACTCCGGAAGCCCTTCATTTC 174
QY 103 ValThAlaThraNpheCySPProAnPheAlaLeuProAnbAnbAnsg1yG1yTP 122
DB 175 GTACCGCCCAACCACTTGTCCCTCCCACTGCTGAGCCGACGACCAATGCGGTGG 234
QY 123 CyAsnProProLeuLysHisPheAspMetAlaGlnProAlaTPG1uLys1leG1y1le 142
DB 235 TGCACCTCTCCCGAGCCACTTGAGCTTCCGATGCCATGTTCTCAAGATCGCCGAG 294
QY 143 TYrArg1yG1y1leValProValLeuPheGlnArgValProCyS1yS1yS1yS1yG1y1y 162
DB 295 TACAAAGCCGGAATCGTCCCGCTCTTACCGCGCGGTCCATGCGTAAAGAAAGGGTGG 354
QY 163 ValArgPheSerValaAng1yArgAspTYrPheG1uLeuValLeu1leSerAnValG1y 182
DB 355 ATCAGGTTTCACATCAACGCGCCACAGTACTTCAACTGCTTGTGATCACCAAGTGGC 414
QY 183 G1yAlaG1ySer1leG1nSerValPhe1leYsg1ySer1yThrG1yTPMetAlaMet 202
DB 415 GGGCAGGGGATATCGTGAAGGTGAGGTGAAGGACCAACCGGGTGGATGCCAATG 474
QY 203 SerArgAsnTPG1ySerAsnTPG1n 211

```

```

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 537 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..537
;   OTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5

Alignment Scores:
Pred. No.: 4,83e-69 Length: 537
Score: 678.50 Matches: 121
Percent Similarity: 78.21% Conservative: 19
Best Local Similarity: 67.60% Mismatches: 36
Query Match: 48.36% Indels: 3
DB: 2 Gaps: 2

US-10-660-499a-2 (1-255) x US-08-845-539-5 (1-537)
QY 34 AATThrPheTyrGlyGlySerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGly 53
DB 7 GCACCTTTATGAGAGGAGCGATGCTTCGGAACCATGGTGCTGTGTGGATGGC 66
QY 54 AsnLeuTyrAlaThrGlyTyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsn 73
DB 67 AATCTTACAGCAGGAGGCTATGGCGTCAACACAGCTGCTTATGACTGCTTCTTCCAC 126
QY 74 AspGlyAlaSerCysGlyGlyCysTyrTyrLeuLeuLeuCysAspTyrLysSerAspSerArg 93
DB 127 AATGGCTCAGCTGTGTGCTGCTTGAATCAAGTGT-----GCTATAGACCTCGA 180
QY 94 TTPCySILeLysGlyArg---SerValThrValThrAlaThrAsnPheCysProProAsn 112
DB 181 TGGTGCCATCTGGTAGCCCTTGATCTTCACTTACCGCTACCAATTTTGTCCCTAAC 240
QY 113 PheAlaLeuProAsnAsnAsnGlyGlyTTPCyAsnProProLeuLysHisPheAspMet 132
DB 241 TTTGCTCTTCCATATACATAGCGGTGGTGTGTAACCTTCTCGACTCATTTTCAGCTTC 300
QY 133 AlaGlnProAlaTTPGlyLysIleGlyIleTyrArgGlyGlyIleValProValLeuPhe 152
DB 301 GCTATGCCATATGTTCTCAAGATCGCTGAGTACCGCGCTGGAATCGAAGCTGTCTCTAC 360
QY 153 GlnArgValProCysLeuLysHisGlyGlyValArgPheSerValAsnGlyArgAspTyr 172
DB 361 CGCCGGGTTCCATGTAGAAACAGAGGAGATCAGGTTCAATCAACGGTTCCGTTAC 420
QY 173 PheGluLeuValLeuIleSerAsnValGlyGlyAlaGlySerIleGlnSerValPheIle 192
DB 421 TTCATATTGTGTATATCAACACGTCGCGGTGAGGGGATTCCTGAGGCTCAACGTA 480
QY 193 LysGlySerLysThrGlyTTPMetAlaMetSerArgAsnTTPGlySerAsnTTPGln 211
DB 481 AAAGATCAACACCGGTTGATGAGCATGATGTAATTGGGGCCAAAACTGGCAG 537

RESULT 9
US-09-362-642-5
; Sequence 5, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; TITLE OF INVENTION: to Control Fruit Texture and Softening
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
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; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
US-09-362-642-5

Alignment Scores:
Pred. No.: 4,83e-69 Length: 537
Score: 678.50 Matches: 121
Percent Similarity: 78.21% Conservative: 19
Best Local Similarity: 67.60% Mismatches: 36
Query Match: 48.36% Indels: 3
DB: 2 Gaps: 2

US-10-660-499a-2 (1-255) x US-09-362-642-5 (1-537)
QY 34 AATThrPheTyrGlyGlySerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGly 53
DB 7 GCACCTTTATGAGAGGAGCGATGCTTCGGAACCATGGTGCTGTGTGGATGGC 66
QY 54 AsnLeuTyrAlaThrGlyTyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsn 73
DB 67 AATCTTACAGCAGGAGGCTATGGCGTCAACACAGCTGCTTATGACTGCTTCTTCCAC 126
QY 74 AspGlyAlaSerCysGlyGlyCysTyrTyrLeuLeuLeuCysAspTyrLysSerAspSerArg 93
DB 127 AATGGCTCAGCTGTGTGCTGCTTGAATCAAGTGT-----GCTATAGACCTCGA 180
QY 94 TTPCySILeLysGlyArg---SerValThrValThrAlaThrAsnPheCysProProAsn 112
DB 181 TGGTGCCATCTGGTAGCCCTTGATCTTCACTTACCGCTACCAATTTTGTCCCTAAC 240
QY 113 PheAlaLeuProAsnAsnAsnGlyGlyTTPCyAsnProProLeuLysHisPheAspMet 132
DB 241 TTTGCTCTTCCATATACATAGCGGTGGTGTGTAACCTTCTCGACTCATTTTCAGCTTC 300
QY 133 AlaGlnProAlaTTPGlyLysIleGlyIleTyrArgGlyGlyIleValProValLeuPhe 152
DB 301 GCTATGCCATATGTTCTCAAGATCGCTGAGTACCGCGCTGGAATCGAAGCTGTCTCTAC 360
QY 153 GlnArgValProCysLeuLysHisGlyGlyValArgPheSerValAsnGlyArgAspTyr 172
DB 361 CGCCGGGTTCCATGTAGAAACAGAGGAGATCAGGTTCAATCAACGGTTCCGTTAC 420
QY 173 PheGluLeuValLeuIleSerAsnValGlyGlyAlaGlySerIleGlnSerValPheIle 192
DB 421 TTCATATTGTGTATATCAACACGTCGCGGTGAGGGGATTCCTGAGGCTCAACGTA 480
QY 193 LysGlySerLysThrGlyTTPMetAlaMetSerArgAsnTTPGlySerAsnTTPGln 211
DB 481 AAAGATCAACACCGGTTGATGAGCATGATGTAATTGGGGCCAAAACTGGCAG 537

RESULT 10
US-08-845-539-3
; Sequence 3, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

```

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298, 829
FILING DATE: 19-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/885,970
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Goseypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
LIBRARY: EMBL-SI
CLONE: SIB12
US-08-298-829-26

Alignment Scores:
Pred. No.: 1,02e-76 Length: 2415
Score: 753.50 Matches: 147
Percent Similarity: 65.81% Conservative: 32
Best Local Similarity: 54.04% Mismatches: 37
Query Match: 53.71% Indels: 56
DB: 2 Gaps: 4

US-10-660-499A-2 (1-255) x US-08-298-829-26 (1-2415)
QY 31 Aenlaahlsalathrphetyrglyserhspalaserglythrmel----- 46
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Db 862 AATGCCCATGCACCTTCTACGCGTGCTGCTATGCTACCGGACAAATGGTGAGTTCAA 921
|||
QY 46 ----- 46
Db 922 ACTTCAACCATTAACCTACATAAAATCTCAGCGTATGTTCTTAATTGTGATGTTTC 981
|||
QY 47 ----GlygIyAlaCygsgIyTyrGlyAsnLeuTyrAlaThrGlyTyrGlyThrArgThrAl 65
Db 982 TATAGGGGAGAGCTTGTGTTATGAAAACCTGTACAGTCAAGGGATGTGAACGAGCAGC 1041
|||
65 aAlaleuSerThrAlaleupheAsnApGlyAlaserGlygIyGlnCySyrIyrlYsIleI 85
|||

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[illegible]

Db 1393 AAAGAGGATCATGATACCATGATGACATTCTGACTTCAACATGCTGTGATAC 1452
Qy 180 AenValGlyValAglSerIleGlnSerValPheIleYsglySerIleYThr 199
Db 1453 AACGTGGAGGGGACGAGGATATACGTCAGTGCATCAAGTGTTCCAAACAGGATGG 1512
Qy 200 MetAlaMetSerArgAntTpgIySerAntTpgIlnSerAntIaTyrLeuAnGlyIn 219
Db 1513 CTACCTATGTCGAAATGGGGCCAAACCTGGACAGCAATGCTTAACCTTAACGGCCAA 1572
Qy 220 SerLeuSerPheArgValThrThrThrAspGlyGluThrArgValPheGlnAplleVal 239
Db 1573 AGCTCTCTTTCAAGTGAATGCGACGAGATGGCAGACTATCAACAACATCAATGTAGTG 1632
Qy 240 ProValSerTprThrPheGlyGlnThrPhe 249
Db 1633 CTGCTGCTTGGCAATTCGACAAACTTTT 1662

RESULT 6
US-08-298-687A-26
; Sequence 26, Application US/08298687A
; Patent No. 5521078
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal B.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,687A
; FILING DATE: 04-OCT-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium barbadense
; STRAIN: Sea Island
; IMMEDIATE SOURCE:
; LIBRARY: EMBL-61
; CLONE: STB12
US-08-298-687A-26

Alignment Scores:

Pred. No.: 1,02e-76 Length: 2415
Score: 753.50 Matches: 147
Percent Similarity: 65.81% Conservative: 32
Best Local Similarity: 54.04% Mismatches: 37
Query Match: 53.71% Indels: 56
DB: 2 Gaps: 4

US-10-660-499a-2 (1-255) x US-08-298-687A-26 (1-2415)

Qy 31 AenValHisAlaThrPheTyrGlyIySerAspAlaSerGlyThrMet----- 46
Db 862 AACTGCCCATGACCTTTACGTGTGTGCTGATGCTACCGGACAAATGGGTGATTCA 921
Qy 46 ----- 46
Db 922 ACTTTCAACCATTAACCTACATATAAATCTAGGCTATGTTCTTAATTTGATGTTTC 981
Qy 47 ----GlyGlyValAcyGlyTyrGlyValMetTyrAlaThrGlyTyrGlyThrArgThrAl 65
Db 982 TATAGGGAGAGCTTGTTGTTATGAAACCTGTACAGTCAAGGTTATGAAACGACACAGC 1041
Qy 65 aAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCyGly-GlnCyTyrIleI 85
Db 1042 AGCTTTAGAGCACTGCACTTTTCAACATGCTTGACCTGGGTGCACTGCTACAGCTGC 1101
Qy 85 leCyAspTyrIySerAspSerArgTyrCyIleIyGlyArgSerValThrValThrA 105
Db 1102 GGTGCAAC-----AATGATCCCTCAATGGTGCAATT--AGTCGAAACCAATACCGTGACG 1152
Qy 105 laThrAsnPheCyPProPheAsnPheAlaLeuProAsnAsnAnGlyIyTTPCyAsp 125
Db 1153 CCACCAACTTTTGTCCCTCACTATGCTTATCTAGTACAGAGCGGGGTGGGCAATC 1212
Qy 125 roProLeuYshIspheAspMetAlaGlnProAlaTpgIuYsIleGlyIleTyrArg 145
Db 1213 CCCACGAGAAACACTTTGATTTTGGCCGAACCGGCACTTTGACAGATCGGGATATCGAG 1272
Qy 145 lyGlyIleValProValIleuPhe-Gln----- 153
Db 1273 CTGGAATGTCCTCCTGTATGTTCAGAAAGTGGTAATAAACAATTCAAATCATCAC 1332
Qy 154 -----ArgValProCyIyIy 159
Db 1333 CTCTTAAGATATGTTAAACGTGGGCTGTAACTTTTGACGGGTGCATGTGTGAAG 1392
Qy 160 HisGlyGlyValArgPheSerValaenGlyArgAspTyrPheGluLeuValIleSer 179
Db 1393 AAAGAGGATCATGATACCATGATGACATTCTGACTTCAACATGCTGTGATAC 1452
Qy 180 AenValGlyValAglSerIleGlnSerValPheIleYsglySerIleYThr 199
Db 1453 AACGTGGAGGGGACGAGGATATACGTCAGTGCATCAAGTGTTCCAAACAGGATGG 1512
Qy 200 MetAlaMetSerArgAntTpgIySerAntTpgIlnSerAntIaTyrLeuAnGlyIn 219
Db 1513 CTACCTATGTCGAAATGGGGCCAAACCTGGACAGCAATGCTTAACCTTAACGGCCAA 1572
Qy 220 SerLeuSerPheArgValThrThrThrAspGlyGluThrArgValPheGlnAplleVal 239
Db 1573 AGCTCTCTTTCAAGTGAATGCGACGAGATGGCAGACTATCAACAACATCAATGTAGTG 1632
Qy 240 ProValSerTprThrPheGlyGlnThrPhe 249
Db 1633 CTGCTGCTTGGCAATTCGACAAACTTTT 1662

RESULT 7
US-08-298-829-26
; Sequence 26, Application US/08298829
; Patent No. 5620882
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal B.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER

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QY 21 -----ThyralapheserProserglyTyrThrAsnAlaHisAlaThrPhe 36
DB 88 GAAGAGAGATCCCTGGTGTATCTGGTGTTCATGGAAACAGCAATGCTACATTT 147
QY 37 TYRGLYGLYSerAspAlaSerGlyThrMetGlyValaCysGlyTYRGLYAsnLeuTYR 56
DB 148 TACGGCGGAAGTATCTCTTGAACAATGGGGCGGTGGTATGGAATTTATAC 207
QY 57 AlaThrGlyTYRGLYThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAla 76
DB 208 AGCAGAGATACGAGATTAAACAGACGACATGATGCTCTTTGTTAAACATGATTA 267
QY 77 SerCysGlyGlnCysTyrIleIleCysAspTyrLysSerAspSerArgTyrCysIle 96
DB 268 AGTTTGAGAGCCGTTTGAATTAATGTAACAATAATCTCTTAATTGAAATGCTGCTT 327
QY 97 LysGlyArg---SerValThrValThrAlaThrAsnPheCysProPheAsnAlaLeu 115
DB 328 CCGGAAACCCCTTCATTTTAATCAACGCTACCAATTTTCCCAACCAATTAACGGCTTG 387
QY 116 ProAsnAsnAsnGlyGlyTyrCysAsnProProLeuLysHisPheAspMetAlaGlnPro 135
DB 388 CCAATGACATGATGCTGCTGTGTAAACCTCTCGCCCTCACTTGACCTCGCTATGCGCT 447
QY 136 AlaTrpGlyLysIleGlyIleTyrArgGlyValIleValProValLeuPheGlnArgVal 155
DB 448 ATGTTTCTCAAACTTCTCAAGTACCGCGCTGGATGTTCTTCACTTAATCGACAGATC 507
QY 156 ProCysLysLysHisGlyGlyValaArgPheSerValaAsnGlyArgAspTyrPheGlnLeu 175
DB 508 CCAATGCGAAGACAGAGATCAAGTTTACATCAATGATTCCTTCACTTCACTTA 567
QY 176 ValLeuIleSerAsnValaGlyValaGlySerIleGlnSerValPheIleLysGlySer 195
DB 568 GTGTTATCATCAATGATGACAGGTGACGGGATATTATTAAGTTGGTAAAGAACAC 627
QY 196 LysThrGlyTyrMetAlaMetSerArgAsnTyrGlySerAsnTyrGlnSerAsnAlaTyr 215
DB 628 AAGACAAATGATGATTCATTAAGCCGTAAATGAGGACAAATATGGCAATCAATGCGGT 687
QY 216 LeuAsnGlyGlnSer 220
DB 688 TTAAGTGTCAATCA 702

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RESULT 5
US-07-885-970A-26
Sequence 26, Application US/07885970A
Patent No. 5495070
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,970A
FILING DATE: 19920518
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 07/253,243
/ FILING DATE: 04-OCT-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27,386
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 283-2478
/ TELEFAX: (608) 251-5139
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2415 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Gossypium barbadense
/ STRAIN: Sea Island
/ IMMEDIATE SOURCE:
/ LIBRARY: EMBL SI
/ CLONE: SIB12
/
US-07-885-970A-26

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Alignment Scores:

Pred. No.:	1,02e-76	Length:	2415
Score:	753.50	Matches:	147
Percent Similarity:	65.81%	Conservative:	32
Best Local Similarity:	54.04%	Mismatches:	37
Query Match:	53.71%	Indels:	56
DB:	2	Gaps:	4

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US-10-660-499a-2 (1-255) x US-07-885-970A-26 (1-2415)
QY 31 AsnAlaHisAlaThrPheTyrGlyLysSerAspAlaSerGlyThrMet----- 46
DB 862 AACTGCCATGACACTTTTACAGGTGGTGTGATGCTACCGGACAAATGGGTGATTCAA 921
QY 46 ----- 46
DB 922 ACTTCAACATTAACCTTACATTAATAATCTAGGCTATGTTCTTAATTGGAGTTTC 981
QY 47 ----GlyGlyAlaCysGlyTyrGlyLysLeuTyrAlaThrGlyTyrGlyThrArgThrAl 65
DB 982 TATAGGGGAGGCTGTGTATGAAACCTGTACAGTCAAGGTATGAAACAGACACAGC 1041
QY 65 AlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGly-GlnCysTyrLysIle 85
DB 1042 AGCTTTGACATGACCTTTTCAACAAATGGCTGAGCTCGGTCAGCTGACGAGCTCC 1101
QY 85 LeCysAspTyrLysSerAspSerArgTyrCysGlyIleLysGlyArgSerValThrAlThr 105
DB 1102 GGTGCAAC-----AATGATCTCTCAATGATGATTT---AGTGCACCAATACCGTACAG 1152
QY 105 LaThrAsnPheCysProPheAsnAlaLeuPheAsnAsnGlyGlyTyrCysAsp 125
DB 1153 CCACCAACTTTGTCCCTTCACTATGCTTTATCTAGTACATAGCGGGGTGGCAATC 1212
QY 125 roProLeuLysHisPheAspMetAlaGlnProAlaTrpGlyLysIleGlyIleTyrArg 145
DB 1213 CCCACAGAAACACTTTGATTTGGCCGAACCGCATTTTGCAAGATGGGGAATATCGAG 1272
QY 145 LysGlyIleValProValLeuPhe-Gln----- 153
DB 1273 CTGGAATCGTCCCTGTATGTTCAAGAGGTGTGATTAACATCAATTCATCATCACA 1332
QY 154 -----ArgValProCysLysLys 159
DB 1333 CTCTTAAGGTATGTTAACTGTGGGTGTTTAACTTTTGACAGGATGATGATGAG 1392
QY 160 HisGlyGlyValaArgPheSerValaGlnGlyArgAspTyrPheGlnLeuValLeuIleSer 179

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QY 248 ThrpheSerSerProValGlnphe 255
DB 661 ACCTATGAAGGCCCT---CAATTC 681

RESULT 3
US-09-362-642-1
; Sequence 1, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum cv. T5
; NAME/KEY: CDS
; LOCATION: (28)..(702)
; OTHER INFORMATION: tomato expansin (Lex1)
US-09-362-642-1

Alignment Scores:
Pred. No.: 2,86e-79 Length: 702
Score: 768.50 Matches: 136
Percent Similarity: 74.22% Conservative: 31
Best Local Similarity: 60.44% Mismatches: 53
Query Match: 54.78% Indels: 5
DB: Gaps: 2

US-10-660-499a-2 (1-255) x US-09-362-642-1 (1-702)
QY 1 MetGlyLysIleuValLeuGlySerIleuGlyLeuGlyCysGlyPheThrIleThr 20
DB 28 ATGGGTATCATATTTTCATCTGTTCTTTTGTGTAGACATCATGTTTCAACATTTGTT 87
QY 21 -----ThrTyrAlaPheSerProSerGlyTyrPheAsnAlaHisAlaThrPhe 36
DB 88 GAAGAAGATCCCTGGTGTACTCTCGGTTCATGGAAGAACTGCACATGCTACATTT 147
QY 37 TyrGlyGlySerAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyr 56
DB 148 TACGGCGGAAGTATGCTTCTGGAACAATGGCGGTGCGTGTGTATGGAATTTATATC 207
QY 57 AlaThrGlyTyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnArgGlyAla 76
DB 208 AGCCAAGATACGAGATTAAACAGACGACCTAAGTACTCTTTGTTTAACAATGATTA 267
QY 77 SerCysGlyGlnCysTyrIleIleCysAspTyrIleSerAspSerAspGlyTyrCysIle 96
DB 268 AGTTTGAGACCTCTTTTGAACCTTAATGACAAATCTCTTAATGGAATGCTGCTT 327
QY 97 LysGlyArg---SerValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeu 115
DB 328 CTGGAACCCCTTCATTTTAAATCAACAGTACCAATTTTGCACCAATTAACGCGTGG 387
QY 116 ProAsnAsnAsnGlyGlyTyrPyrAsnProProLeuIleHisPheAspMetAlaGlnPro 135
DB 388 CCAAAATGACATATGCTGCTGTGTAACTCTCGCCCTCACTTGTGCTGCTAGTCCCT 447
QY 136 AlaTyrGlyLysIleGlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgVal 155
DB 448 ATGTTTCTCAAACTTGCTACGTACCGGCTGGCATTTTCTCTGTAATTATCCAGAGATC 507
QY 156 ProCysLysLysHisIleGlyIleValArgPheSerValAsnGlyArgAspTyrPheGlnLeu 175
DB 688 TTAAGTGTCAATCA 702

RESULT 4
US-08-845-539-1
; Sequence 1, Application US/08845539
; Patent No. 5928303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..702
; OTHER INFORMATION: /product= "tomato Lex1"
US-08-845-539-1

Alignment Scores:
Pred. No.: 1.08e-78 Length: 702
Score: 763.50 Matches: 135
Percent Similarity: 73.78% Conservative: 31
Best Local Similarity: 60.00% Mismatches: 54
Query Match: 54.42% Indels: 5
DB: Gaps: 2

US-10-660-499a-2 (1-255) x US-08-845-539-1 (1-702)
QY 1 MetGlyLysIleuValLeuGlySerIleuGlyLeuGlyCysGlyPheThrIleThr 20
DB 28 ATGGGTATCATATTTTCATCTGTTCTTTTGTGTAGACATCATGTTTCAACATTTGTT 87
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TOPOLOGY: UNKNOWN			
US-08-440-517A-1			
Alignment Scores:	3.21e-93		
Pred. No.:	889.00		
Percent Similarity:	80.70%		
Best Local Similarity:	68.42%		
Query Match:	63.36%		
DB:	2		
US-10-660-499A-2 (1-255) x US-08-440-517A-1 (1-681)			
QY	28	GIYTPTRhsmAlahIsalathrPheTYrGlyGlySerAspAlaSerGlyThrMetGly	47
DB	10	GGCTGGCAGAGCGGCGCACGCCACCTTTATGGTGGTGGACCGACATCGGCACATGGGT	69
QY	48	GIYAlaCYSGIYTYrGlyAsnLeuTYrAlaThnGlyTYrGlyThraTrgThraIaaIaLeu	67
DB	70	GGAGCTGTGGGTATGGGAATTTATACAGCCAAAGGTATGGCACGAAACAGGTGGGGCTG	129
QY	68	SeThrAlaLeuPheAsnAspGlyAlaSerCYSGIYgInCYseTYrIysIleIeCYasp	87
DB	130	AGCATCGGCTATTTAACAATGATTAAGTGTGGTGCTTGTCGAATAAGACTTG---	186
QY	88	TYrLYSerAspSerArgTYrCYsIleLYSGIYArgSerValThrValThraIaThraSn	107
DB	187	---ACAAACGACCCCTTAATGTGCTTCGCGGGA---ACTATTGGGTCACTGCCACCAAC	240
QY	108	PheCYseProProAsnPheAlaLeuProAsnAsnAngIYgIYTPCYsAsnProProLeu	127
DB	241	TTTTGGCCCTCAACTTGTCTCTCCCTTAACAACAATGGTGGATGGCAACCTCTCTC	300
QY	128	LYSHIePheAspMeAlaGInProAlaTrpGluLYseIleGlyIleTYrArgIYgIYIle	147
DB	301	CAACACTTGACATGGCTAGCCTGCTTCCTTCAATGCTCAATAACGAGCTGGATTC	360
QY	148	ValProValLeuPheGInArgValProCYsLYSHIeGlyIYgIYValArgPheSerVal	167
DB	361	GGCCCGCTCTCTTGTGGAGGATCAATGATGAAGAAAGGTGAGTGAAGGTTCATATC	420
QY	168	AngIYArgAspTYrPheGluLeuValIleIeSerAsnValGlyGlyIaGlySerIle	187
DB	421	AATGGCACTCACTACTCAACCTCGTTTGATCAAAACGTGGTGGCGAGCGACATC	480
QY	188	GInSerValPheIleLYSGIYSerLYSThrGlyTYrMeAlaMetSerArgAsnTrpGly	207
DB	481	CACTCTGTTCGATTAAGGGGTTCGAACCTGGATGGCAATCATGTCTAGAAATTGGGC	540
QY	208	SeArgnTrpGInSerAsnAlaTYrLeuAsnGlyGInSerLeuSerPheArgValThrThr	227
DB	541	CAAACTGGCAAAAGCAACAATATCTCAATAGGCCAAGGCTTCTCTTCAAGCACTCT	600
QY	228	ThraSPGlyGluThraArgValPheGInAspIleValProValSerTrpThrPheGlyGIn	247
DB	601	AGTGAATGTGTGCGCACTCACTGCTTAATCTGTCTTCAATTGGCAATTGGCCAA	660
QY	248	ThraPheSerSerProValGInPhe	255
DB	661	ACCTATGAAGGCCCT---CAATTC	681
RESULT 2			
US-09-092-160-1			
Sequence 1, Application US/09092160C			
Patent No. 6255466			
GENERAL INFORMATION:			
APPLICANT: Cosgrove, Daniel J			
APPLICANT: McQueen-Mason, Simon			
APPLICANT: Guiltinan, Mark J			
APPLICANT: Shcherban, Tatyana			
APPLICANT: Shi, Jun			
FILE OF INVENTION: PURIFIED EXPANSIN PROTEINS			
FILE REFERENCE: 1194/1C114US3			

[illegible]

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2006, 21:35:05 ; Search time 185 Seconds

(without alignments)
2450.153 Million cell updates/sec

Title: US-10-660-499A-2

Sequence: 1 MGKIMLVLSLIGLCCFTT.....QDIVPVSWTFGRFSSPVQF 255

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Ygapopt 10.0	Ygapext 0.5	
Fgapopt 6.0	Fgapext 7.0	
Delopt 6.0	Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	889	63.4	681	2	US-08-440-517A-1
2	889	63.4	681	3	US-09-092-160-1
3	768.5	54.8	702	3	US-09-362-642-1
4	763.5	54.4	702	2	US-08-845-539-1
5	753.5	53.7	2415	2	US-07-885-970A-26
6	753.5	53.7	2415	2	US-08-298-687A-26
7	753.5	53.7	2415	2	US-08-298-829-26
8	678.5	48.4	537	2	US-08-845-539-5
9	678.5	48.4	537	3	US-09-362-642-5

10	618.5	44.1	501	2	US-08-845-539-3	Sequence 3, Appli
11	618.5	44.1	501	2 <th>US-09-362-642-3</th> <th>Sequence 3, Appli</th>	US-09-362-642-3	Sequence 3, Appli
12	586	41.8	727	2 <th>US-07-885-970A-6</th> <th>Sequence 6, Appli</th>	US-07-885-970A-6	Sequence 6, Appli
13	586	41.8	727	2 <th>US-08-298-687A-6</th> <th>Sequence 6, Appli</th>	US-08-298-687A-6	Sequence 6, Appli
14	586	41.8	727	2 <th>US-08-530-797-5</th> <th>Sequence 6, Appli</th>	US-08-530-797-5	Sequence 6, Appli
15	586	41.8	727	2 <th>US-08-298-829-6</th> <th>Sequence 6, Appli</th>	US-08-298-829-6	Sequence 6, Appli
16	586	41.8	727	2 <th>US-08-787-335-5</th> <th>Sequence 6, Appli</th>	US-08-787-335-5	Sequence 6, Appli
17	302.5	21.6	760	3 <th>US-09-071-252-1</th> <th>Sequence 1, Appli</th>	US-09-071-252-1	Sequence 1, Appli
18	291.5	20.8	819	3 <th>US-09-071-252-8</th> <th>Sequence 8, Appli</th>	US-09-071-252-8	Sequence 8, Appli
19	266.5	19.0	279	3 <th>US-09-313-294A-1276</th> <th>Sequence 1276, Ap</th>	US-09-313-294A-1276	Sequence 1276, Ap
20	258.5	18.4	999	3 <th>US-09-071-252-2</th> <th>Sequence 2, Appli</th>	US-09-071-252-2	Sequence 2, Appli
21	258	18.3	1392	3 <th>US-09-071-252-5</th> <th>Sequence 5, Appli</th>	US-09-071-252-5	Sequence 5, Appli
22	257	18.3	1004	3 <th>US-09-071-252-3</th> <th>Sequence 3, Appli</th>	US-09-071-252-3	Sequence 3, Appli
23	243	17.3	1072	2 <th>US-07-971-096-1</th> <th>Sequence 1, Appli</th>	US-07-971-096-1	Sequence 1, Appli
24	243	17.3	1072	2 <th>US-08-175-096-1</th> <th>Sequence 1, Appli</th>	US-08-175-096-1	Sequence 1, Appli
25	241	17.2	1378	3 <th>US-09-071-252-4</th> <th>Sequence 4, Appli</th>	US-09-071-252-4	Sequence 4, Appli
26	234.5	16.7	759	3 <th>US-08-441-507-20</th> <th>Sequence 20, Appl</th>	US-08-441-507-20	Sequence 20, Appl
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28	232.5	16.6	810	3 <th>US-08-413-974-5</th> <th>Sequence 5, Appli</th>	US-08-413-974-5	Sequence 5, Appli
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33	232.5	16.6	810	3 <th>US-07-971-096-3</th> <th>Sequence 3, Appli</th>	US-07-971-096-3	Sequence 3, Appli
34	232.5	16.6	1123	2 <th>US-08-175-096-3</th> <th>Sequence 3, Appli</th>	US-08-175-096-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-08-440-517A-1
; Sequence 1, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SHCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE

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 Db 184 AAGTGTGAGCAAGAAAGATGATCTGTCACCACTACTGCAACAACTTCTGCTCTTAAC 243
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 DEFINITION AF332171
 ACCESSION AF332171
 VERSION AF332171.1 GI:14193754
 KEYWORDS
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 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1031)
 REFERENCE Wu, Y., Mealey, R.B. and Cosgrove, D.J.
 Analysis and expression of the alpha-expansin and beta-expansin
 gene families in maize
 Plant Physiol. 126 (1), 222-232 (2001)
 JOURNAL PUBMED 11351085
 2 (bases 1 to 1031)
 REFERENCE Wu, Y., Mealey, R.B. and Cosgrove, D.J.
 Direct Submission
 Submitted (27-Dec-2000) Biology, Penn State University, 208 Mueller
 Lab, University Park, PA 16802, USA
 JOURNAL Location/Qualifiers
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Search completed: January 11, 2006, 13:28:06
 Job time : 5618 secs

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

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Location/Qualifiers
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RESULT 14

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ACCESSION AJ623308
VERSION AJ623308.1 GI:58333697
KEYWORDS exp gene; expansin.
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa.
1

REFERENCE

AUTHORS Saiprasad,G.V.S. and Lalitha,A.
TITLE Isolation, cloning and characterization of alpha-expansin gene from banana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 539)
AUTHORS Saiprasad,G.V.S.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-2004) Saiprasad G.V.S., Biotechnology, Indian Institute of Horticulture Research, Heesaraghatta Lake Post, Bangalore, Karnataka 560089, INDIA

FEATURES

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gene
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ORIGIN

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Matches 423; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
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DB 4 CATGCAACTTTCTACCGCGGACAGATGCACTGAGAACTATGGGGGAGCTGTGTAT 63
QY 208 GGGAACTGTATGCAACTGCGGTATGGAACATGGAACCTTAAAGCACTGCTTATTT 267
DB 64 GGTATCTATATTTCTACTGCGGTACGGAACAGACTGCTCTTACACTGCTTATTT 123

Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
 Direct Submission
 Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
 3 (bases 1 to 759)
 Toriumi, M., Wong, C., Hanan, V.W., Onodera, C.S., Quach, H.L., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tridip, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
 Direct Submission
 Submitted (07-MAY-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
 Annotation based on July 2002 version of the Arabidopsis genome
 submitted to Genbank.
 Location/Qualifiers
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 236 CTAGAACTGACGCTTATGACATGCTTATTTATATGATGAGCTTCTGTGTGCTAGTCT 295
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 296 ACAAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 355
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 416 GGTGCAACCAACCACTCAAGACATTTATATGATGAGCCCAACCGGCTTGGAAAAAGTTGTA 475
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 476 TTTAACAAGAGGAGATGTCCTCCGCTGATTTCAAAAGGTTCAATGAAAAAGATGAG 535

Db 416 TTACAGAGAGAAATCGTCCGTCGTTTCCAAAGAGTATGATGATGATGATGATG 475
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 Qy 536 GGTATGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 595
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 Db 476 GAGTTAGATTCGAATTAACGAAGAGACTTCTGAGTATGATGATGATGATGATG 535
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 Qy 596 GGGGTCTGATTCATTCATGATGATGATGATGATGATGATGATGATGATGATG 655
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 Db 536 GAGGACAGCTTCTATTAATCTGATGATGATGATGATGATGATGATGATGATG 595
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 RESULT 13
 AY080738 1088 bp mRNA linear PLN 15-NOV-2002
 LOCUS Arabidopsis thaliana At1g20190 mRNA sequence.
 DEFINITION AY080738
 ACCESSION AY080738.1 GI:19347856
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
 Rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1088)
 REFERENCE
 AUTHORS
 Yamada, K., Banb, J., Chang, C.H., Chang, B., Dale, J.M.,
 Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.,
 Toriumi, M., Wu, H.C., Yamamura, Y., Yu, S., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
 Arabidopsis Full Length cDNA Clones
 Unpublished
 2 (bases 1 to 1088)
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Yamada, K., Banb, J., Chan, M.M., Chang, C.H., Chang, B., Dale, J.M.,
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
 Direct Submission
 Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banb, J., Chan, M.M., Chang, C.H., Chang, B., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

RESULT 11				
LOCUS	CQ0805880	759 bp	DNA	linear
DEFINITION	Sequence 2291 from Patent WO2004035798.			PAT 10-MAY-2004
ACCESSION	CQ0805880			
VERSION	CQ0805880.1	GI:47111574		
KEYWORDS				
SOURCE				
ORGANISM	Arabidopsis thaliana (thale cress)			
	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1			
AUTHORS	Inze, D., de Veylder, L. and Vlieghe, K.			
TITLE	Identification of novel e2f target genes and use thereof			
JOURNAL	Patent: WO 2004035798-A 2291 29-APR-2004;			
	CropDesign N.V. (BE)			
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Source	Location/Qualifiers			
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	/mol_type="unassigned DNA"			
	/db_xref="caxon:3702"			

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Db	56	ATGGGTTTAGAGCCCTTCGTGTTTAATCTAATGTCACGTAAATCTTATGAGAGAAATGACG	115
Qy	176	CTTCAGAGAACTAATGAGGGGAGACTTGTGGGATATGGGAATCTGTATGCAATCGGATAGAA	235
Db	116	CTTCTGGAACAATGGGTGGAGCTTGTGGTTACGGAAGATCTTTACTGGCGGGGATACGGGA	175
Qy	236	CTAGAACTGACCTTTAAGCACTGCTTATTTAATGATGAGACTTCTGTGTGTCAGTGTCT	295
Db	176	CAATGACGGGGGCTTAAAGCAGCGCTCTGTTCACACGAGAGCTTCTTGGGGAAATGCT	235
Qy	296	ACAAATTAATATGATGATTAACAATACACTGTAGATGATGATGATCAAAAGAAAGATCTGTAA	355
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Qy	356	CCGTAATCTGCACAAATCTTTGCCCCCTCCCAATTTGCGCCCTCTCAACAACAATGAGAGCT	415
Db	296	TTATTAACAGCACTAATCTTTTGGCCACCAACTTTGTTGGCTTAACAACAACGATGTT	355
Qy	476	TTTACAGAGAGAGATGCTGCCCTGTGTATTTTCAAGAGGTTCCATGCAAAAACATGAGAG	535
Db	416	TTTACAGAGAGAGATGCTGCCCTGTGTATTTTCAAGAGGTTCCATGCAAAAACATGAGAG	475
Qy	536	GGGTTAGGTTCAAGTGTAAATGGAGAGGACTACTTGTGAGTATGATCAGCAATGTGG	595
Db	476	GAGTTAGATTCAGAAATTAACGGAAGAGACTTTCAGACTAGTGAATATTCAAAATGTAG	535
Qy	596	GAGGTGTGTGATCATTCATCAATCAGTGTCTATTAAAGCTCAAAAATCGATGATGAGCA	655
Db	536	GAGGAGCAGGTTCTAATTAATCTGTATTCATCAAAAGATCAAGAAGCTGTTGGTTAGCA	595
Qy	656	TGTCAAGAAATTTGGGGTTCATAATTTGGAATTCGAATGCTATTTGAATGTTCATCTTGT	715
Db	596	TGTCTCTTAATCTGGGGAGCTTAATTTGGCAATCGAATGTATTATCTAGATGTGTCAAGCTCTCT	655
Qy	716	CCTTCAAGGGTCAACAACAATCTGATGAGAGACGAGAGTTTCCAAAGATATGTTCAGTTAA	775
Db	656	CTTCTCCATTAACACTACTGATGATGATGCTACTAGAGTCTTCTTCATATGTTGTCTTCTT	715
Qy	776	GTTGACATTCGGGCCAACTTCTCTAGCCCAAGTTCAGTCTTAA	819
Db	716	CTTGTCTTTTGGACAGATTATTTCTTCAACGTTAGTTTAA	759
RESULT 12			
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LOCUS			linear
DEFINITION			Arabidopsis thaliana clone C00124 (e) putative expansin S2
ACCESSION			AF332436
VERSION			AF332436.1
KEYWORDS			GI:12083279
SOURCE			FLI CDNA.
ORGANISM			Arabidopsis thaliana (thale cress)
REFERENCE			Arabidopsis thaliana
AUTHORS			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
			1 (bases 1 to 759)
			Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Che, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tzipi, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
			Arabidopsis Open Reading Frame (ORF) Clones
			Unpublished
			2 (bases 1 to 759)
			Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooker, S., Chao, Q., Chen, H., Karlin-Neuman, G., Kim, C., Lam, B., Miranda, M., Nguyen, M.,

JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genest carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

source

CDS

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ORIGIN

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Query Match      36.1%; Score 393; DB 15; Length 978;
Best Local Similarity 71.6%; Pred. No. 1.1e-68;
Matches 516; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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DB 87 ATTCCTGTGATGGCTTAAGCTCTTGTTAACTAATGACCACTTAACTTAACT 146
QY 166 GGTAGTATGCTTCAGAACTATGCGGGAGCTTGTGGTATGGAACTGTATGCAACT 225
DB 147 GGAAGTACCGCTCTTGAAACAAATGGGTGAGCTTGTGGTATGGAACTGTATGCAACT 206
QY 226 GGGATGGAACCTGAACCTGCACTTTAAGCACTGCTTATTTATGATGAGCTTCTGT 285
DB 207 GGGATGGAACCTGAACCTGCACTTTAAGCACTGCTTATTTATGATGAGCTTCTGT 266
QY 286 GGTGATGCTACAAATTTATATGATTAACAATCAGACTCTGATGGTGCATCAAGA 345
DB 267 GGAAATGCTATGATGAATGATGATCAAGCGCGGCACTCAAGGTGCTGTAAGA 326
QY 346 AGATCTGTAACCGTAACCTGCAAACTTTTCCCTTCCCAATTTCCCTTCTTAAC 405
DB 327 GCTTCGTGTATTAACGACCACTAACCTTTTCCCAAACTTTTCCCTTCTTAAC 386
QY 406 AATGAGAGCTGTGCAACCACTCAAGATTTTATGAGCCCAACCGCTTGGAA 465
DB 387 AATGAGAGCTGTGCAACCACTCAAGATTTTATGAGCCCAACCGCTTGGAA 446
QY 466 AAGATGTAATTTACAGAGAGGAGTGTCCCGGTGCTATTTCAAGGGTTCCATGCA 525
DB 447 AAGATCGGAATTTACAGAGAGGAGTGTCCCGGTGCTATTTCAAGAGTCACTTAC 506
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QY 826 T 826
DB 807 T 807

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RESULT 10
AF291659 1135 bp mRNA linear PLN 24-AUG-2000
LOCUS
DEFINITION Striga asiatica alpha-expansin 3 mRNA, complete cds.
ACCESSION AF291659
VERSION AF291659.1 GI:9887378
KEYWORDS
SOURCE
ORGANISM Striga asiatica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Orobanchaceae; Buchneraceae; Striga.
REFERENCE
1 (bases 1 to 1135)
O'Malley,R.C. and Lynn,D.G.
Expansin Message Regulation in Parasitic Angiosperms: Marking Time
in Development
Plant Cell (2000) In press
2 (bases 1 to 1135)
O'Malley,R.C. and Lynn,D.G.
Direct Submision
Submitted (01-AUG-2000) Chemistry and Biology, Emory University,
Emory Rd, Atlanta, GA 30322, USA
Location/Qualifiers
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CDS

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QY 86 TTGATTTATGCTGTTTCAATCACTAATCACTTCTTCACTTCTGATGAGCAAG 145
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QY 146 CCCATGCACTTTTATGAGGGGATGATGCTTCAAGAACTAATGAGGGGAGCTTGT 205
DB 178 CCCATGCACTTTTATGAGGGGATGATGCTTCAAGAACTAATGAGGGGAGCTTGT 237

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ORIGIN

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Query Match      35.4%; Score 385.8; DB 15; Length 1135;
Best Local Similarity 70.3%; Pred. No. 2.9e-67;
Matches 516; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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 QY 608 CATTCAATACAGTTTCATTAAGCTCATAAATCTGATGAGGAAATGCAAGAAAT 667
 Db 647 CTGTACAATCTGTTCAATTAAGGCTCAAAAACAACGATGACAAATGCTAGAAAT 706
 QY 668 GGGGTTCTAATTTGGCAATCCAAATGCGTATTTGAATGTCATCTTTGCTTCAAGGCTCA 727
 Db 707 GGGGGGCAATTTGGCAATCCAAATGCTATTCATATGTCACCACTTGTCTTTAAGGTCA 766
 QY 728 CACCACTGATGAGAGACCAAGTTTCCAGATATTTGTCAGTAAGTTCACATTCG 787
 Db 767 CTACTACCGAGGCTGACCAAAACATCTTAATATGTTGCTCTCCACTGCAATTTG 826
 QY 788 GCGAACTTCTTACGCCAGTTCAGTTCAT 819
 Db 827 GCGAGACATATTCACCTCTATTATTTCTAA 858

RESULT 4

LOCUS LES560646 1318 bp mRNA linear PLN 09-MAY-2003
 DEFINITION Lycopersicon esculentum mRNA for expansin11 (expi1 gene).
 ACCESSION AJ560646
 VERSION AJ560646.1 GI:30519751
 KEYWORDS exp1 gene; expansin11.
 SOURCE Lycopersicon esculentum (Solanum lycopersicum)
 ORGANISM Lycopersicon esculentum
 Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 Vogler, H. and Mandel, T.
 AUTHORS Vogler, H.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1318)
 AUTHORS Vogler, H.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAY-2003) Vogler H., Biology, University of Berne,
 Altenbergrain 21, Berne, 3013, SWITZERLAND
 FEATURES Location/Qualifiers

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ORIGIN

Query Match 40.0%; Score 435.2; DB 15; Length 1318;
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 Db 124 TTTCGTTAGTACGCAATGCTTCTGCTTCTGATGATGATGCTCATGCTACTTT 183

QY 159 TTATGGGGTAGATGATCTTTCAGAACTATGAGGGAGAGCTTGTGGTATGGAATCTGA 218
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 QY 219 TGGCACTGGGTATGGAATGAACTGACAGCTTTAGCACTGCTTATTAAGATGAGAC 278
 Db 244 CTCMAAGAGTTATGTAACAACAACCTGCAATTAAGTATCTGATGCTTCAATGATGAGAC 303
 QY 279 TTCCTGTGTCAGTGTCAAAATATATGATTAACAATGACACTAGATGATGAT 338
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 Db 364 AAGGGAACATCTATTACAACTACAGCCACTAATTTTTCACCAAAATTTGCACTTCC 423
 QY 399 TAACAACATGAGAGGTGTGCAACCCACATCMAAGCAATTTGATATGAGCCCAACGCC 458
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 QY 459 TTGGGAAAAGATTGATTTTACAGAGAGAGATGCTCCCGTGTATTTCAAAGGTTCC 518
 Db 484 TTGGGAAAAGATTGATTTTACAGAGAGATGCTCCCGTGTATTTCAAAGGTTCC 543
 QY 519 ATGCAAAAAGATGAGAGAGGTTAGTTCAAGTGTGAATGAGAGGACTTGTGAGCTAGT 578
 Db 544 TTGTGTGAAAAGATGAGGATTAAGATTTCAATTAATGAGAGGACTTATTTGAGCTAT 603
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 Db 784 AATGTTGCTTCATCCAAATGAGGATTTGAGCAAAATTTCAAGCTCATTAATTAAT 843
 QY 819 AGCTGATTAAGATTAACCAACCAAGCGCTGAGGCTGCTTTTATTTTATTAAT 874
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RESULT 5

LOCUS AF492631 1133 bp mRNA linear PLN 24-DEC-2002
 DEFINITION Capsicum annuum putative expansin (upa7a) mRNA, complete cds.
 ACCESSION AF492631
 VERSION AF492631.1 GI:20149055

KEYWORDS Capsicum annuum
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 1133)
 AUTHORS Marois, E., Van den Ackereken, G. and Bonas, U.
 TITLE The xanthomonas type III effector protein AvrBs3 modulates plant
 gene expression and induces cell hypertrophy in the susceptible
 host

JOURNAL Mol. Plant Microbe Interact. 15 (7), 637-646 (2002)
 PUBLISHED 12118879
 REFERENCE 2 (bases 1 to 1133)
 AUTHORS Marois, E., van den Ackereken, G. and Bonas, U.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2002) Genetec, Martin-Luther University,
 Weinbergweg 10, Halle 06099, Germany

LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
123	CTCACCTTCTGGAATGGAACAAGCCCAATGCCACTTTTAAATGAGGGGTAAGTAGATGCTCAGG	AF049350	1307 bp	mRNA	linear	PLN 23-APR-2004				
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186	TACAAATGGGGGGTGGCTTGTGATATGAGCACTTGTATTCACAGGGGTATGGAATCTAGAAC	AF049350	1307 bp	mRNA	linear	PLN 23-APR-2004				
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303	TATATGTATTAAACAAATGAGACTCTAGATGGGATCAACAAAGAAAGATCTGTAAACCGTAAAC	AF049350	1307 bp	mRNA	linear	PLN 23-APR-2004				
306	CATTGTGATTTCTATGCAAGAACCGCATGCTGCAAGAGAGAGATCTGTAAACCAATAC	AF049350	1307 bp	mRNA	linear	PLN 23-APR-2004				
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DB	167 CTTCTGATGAGCAAGTGTCTATGCCACTTTTATATGATGATGATGATGATGATGATG 226	
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2006, 10:09:57 ; Search time 5613 Seconds
(without alignments)
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Title: US-10-660-499A-1

Perfect score: 1089

Sequence: 1 gccagagctcaactctca.....aaaaaaaaaaaaaaaa 1089

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	430.2	39.5	1133	15	AF492631 Capsicum
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15	336.4	30.7	1031	15	AF332171 Zea mays
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18	333	30.6	1137	15	AK069548 Oryza sat

19	331	30.4	1355	15	AB196979 Sagittari
20	314.4	28.9	965	15	AY589583 Triticum
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ALIGNMENTS

RESULT 1
AF516879
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF516879 Glycine max expansin (Exp1) mRNA, complete cds.
AF516879
AF516879.1 GI:27464176
Glycine max (soybean)

REFERENCE

1 (bases 1 to 1089)
Lee,D.K., Ahn,J.H., Song,S.K., Choi,Y.D. and Lee,J.S.

AUTHORS

Expression of an Expansin Gene Is Correlated with Root Elongation

TITLE

in Soybean

JOURNAL

Plant Physiol. 131 (3), 985-997 (2003)

REFERENCE

2 (bases 1 to 1089)
Lee,D.-K., Ahn,J.H., Choi,Y.D. and Lee,J.S.

AUTHORS

Submitted (30-MAY-2002) School of Biological Sciences, Seoul

TITLE

National University, Shinrim-dong, Kwanak-gu, Seoul 157-747, Korea

JOURNAL

location/Qualifiers

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RESULT 14
US-10-750-185-57411/c
; Sequence 57411, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57411
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Bovine 19866881260245
US-10-750-185-57411

Alignment Scores:
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Score: 85.00 Matches: 45
Percent Similarity: 39.74% Conservative: 15
Best Local Similarity: 29.80% Mismatches: 58
Query Match: 6.06% Indels: 33
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US-10-660-499A-2 (1-255) x US-10-750-185-57411 (1-1873)
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; Sequence 57411, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57411
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Bovine 19866881260245
US-10-750-623-57411

Alignment Scores:
Pred. No.: 109 Length: 1873
Score: 85.00 Matches: 45
Percent Similarity: 39.74% Conservative: 15
Best Local Similarity: 29.80% Mismatches: 58
Query Match: 6.06% Indels: 33
DB: Gaps: 10

US-10-660-499A-2 (1-255) x US-10-750-623-57411 (1-1873)
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Percent Similarity: 32.79% Conservative: 33
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US-10-660-499a-2 (1-255) x US-11-170-653-10 (1-645)

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RESULT 11
 US-11-121-086-24/C

/ Sequence 24, Application US/11121086
 / Publication No. US20050266459A1
 / GENERAL INFORMATION:
 / APPLICANT: POULSEN, TIM S.
 / APPLICANT: NIELSEN, KIRSTEN V.
 / TITLE OR INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 / FILE REFERENCE: 09138.6000-00000
 / CURRENT APPLICATION NUMBER: US/11/121.086
 / PRIOR FILING DATE: 2005-05-04
 / PRIOR APPLICATION NUMBER: 60/567,570
 / PRIOR FILING DATE: 2004-05-04
 / NUMBER OF SEQ ID NOS: 107

/ SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 24
 / LENGTH: 120096
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-11-121-086-24

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QY 81 -----CyTyrlsIleIleCyAspTyrrlySerAspSerArgr 93
DB 60203 GGGCTGCAATGAGACCGCAGTTCAGAGAG-----TGTTCACACAGCCTTCC 60156
QY 94 TrpCyS-----IleTyrglyArgrSerValThrValThrAla 105
DB 60155 TGGTGCATGGGCTCACTGCTTGGCCAGTGGCTTGGCAGAGGCTTCCCTCCACAGCC 60096
QY 106 ThrAsnPh-----CyS-ProProAsnPhAlaLeuProAsnAs 118
DB 60095 TGCAGGTTCTTATGCGCAGAGCTCCCTTCTTGCCCAACAGAGGCTGTTTTCACAGATA 60036
QY 118 nAsnGlyGlyTrpCyAsnProProLeuIle----- 128
DB 60035 CAGAGGTGGGCGAGATCCAGCCCGTTGAAACAGACAGAGCTTTGGAGGCCACATTGGCG 59976
QY 129 -HisPheAspMetAlaGlnProAlaTrpGlyIleTyArgGlyIleVal 148
DB 59975 CATTCTCAGAGGGGCAAGTGGCTGGGCTGAGCCAGGCACTGAGTGGCCCTTGA 59916
QY 148 lProValLeuPheGlnArgValProCySlyAsnHisgIyGlyValArgPheSerValAs 168
DB 59915 GCCTCTGTGACAGGCTGAGGCCCCCG-----AGGCACTGTGGCTGTGTCACATACA 59862
QY 168 nGlyArgAspTyrrPheGlnLeuValLeuIleSerAsnValGlyAlaGlySerIleGt 188
DB 59861 CAGAGCTGAT-----AAGAGATGAAGTCACTAGATGTGGGGCGGCAACCCCGCCG 59808
QY 188 nSerValPheIleIleGlySerIySerThrGlyTrpMetAlaMetSerArgrAsnTrpIySe 208
DB 59807 GGCTGTGTT-----GAGAGTGGCCCTGTGCTGAGAGCC 59775
QY 208 rAsnTrpGlnSerAsnAla 214
DB 59774 AGCTTGCCCTGAGACGCT 59756

```

RESULT 12

US-11-128-061-872/C
 / Sequence 872, Application US/11128061
 / Publication No. US20060003958A1
 / GENERAL INFORMATION:
 / APPLICANT: Melville, Mark W.
 / APPLICANT: Charlebois, Timothy S.
 / APPLICANT: Mounts, William M.
 / APPLICANT: Hann, Louane E.
 / APPLICANT: Sinacore, Martin S.
 / APPLICANT: Leonard, Mark W.
 / APPLICANT: Brown, Eugene L.

```
Db 354 TACTGGAACCTATTAAGTACTGTA-----AAAAG 383
Qy 159 shisgilygY-----ValArgphe-----SerValangl 169
Db 384 TGATGGGGGTACATATGACATATATACACTACGCTTATACGACCTTCATTTGATGG 443
Qy 169 Y-----ArgAspTYrPhegluValleuValleuIleSerValglgylal 164
Db 444 CGATCGCACTACTTTTACGACGAGTACTGAGT-----GTTCCGACGTCGAAGACCAAC 497
Qy 184 aglyserIleglSerValPheIlelysglyserlyThrglYTrpMecAlameterar 204
Db 498 CGAAGACGACGTCATACATCACTTCACGACATCATGTACAGCATGAGAGCCATGGAAT 557
Qy 204 gAsnTPglYserAsnTPglInSerAsnAlaTYrLeuAnnglyGlnSerleuSerPhear 224
Db 558 GAATCTGGGCGAGTAATTTGG-----GCTTACCA 584
Qy 224 gValThrThrThraSpglY 230
Db 585 AGTCATGGCGACAGAAAGA 603

RESULT 9
US-10-517-939-223
; Sequence 223, Application US/10517939
; Publication No. US2006003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Beleglialian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-223

Alignment Scores:
Pred. No.: 9.67 Length: 642
Score: 89.00 Matches: 48
Percent Similarity: 32.39% Conservative: 32
Best Local Similarity: 19.43% Mismatches: 88
Query Match: 6.34% Indels: 79
DB: Gaps: 13

US-10-660-499a-2 (1-255) x US-10-517-939-223 (1-642)
Qy 7 ValLeuGlYserLeuIleGlYleuCYsCySphemTrIleThrThrThraLapheSerpr 26
Db 33 ATTATGGGCGAGCTTATAGATATAGCTTGTTCGGCAACCGCTCTGCACTAGCAC 92
Qy 26 oSerGlYTrpThraSnAlaHisAlaThrPheTYrGlYserAspAlaSerGlYThrMe 46
Db 93 AGACTACTGGCAAAAT-----TGACCTGATGGGCGGTATAGT 131
Qy 46 tglYglYAlaCYsGlYTYrGlYAsnLeuTYrAlaThmglYTYrGlYThraThraAla 66
```

```
Db 132 AAACGCTGTCAATGGGTCTGGCGGAATTACAGTGTAAATTGGCTTAAT-----180
Qy 66 aLeuSerThraAlaLeuPheAsnAspGlYAlaSerCYsGlYGlnCYsTYrlyIleleCY 86
Db 181 -ACCGAAATTTGTTGTTGTTAAAGTTTGACATACAGGTTCCCATTTTGAAGATGA-- 237
Qy 86 sAspTYrlySerAspSerArgTrpCYrIlelysglyArgSerValThraThraIath 106
Db 238 -AACTTAATGCC--CGAATTGGGCA-----261
Qy 106 rAsnPheCYsProProAsnPheAlaLeuProAsnAsnngly-----G1 121
Db 262 -----CCGAATGCAAAATGCAATTTAACTTATATATGG 293
Qy 121 YTrpCYsAsnProProLeuLYshIsPheAspMecAlaGlnPro-----AlaTrpGlY 139
Db 294 TTGAGAGATCACTCTCTCATAGATATATATGATGAGATTCATGGGCTACTATATGACC 353
Qy 139 sIleGlYIleTYrArgGlYglYIleValProValleuPheGlnArgValProCYslyly 159
Db 354 TACTGGAACGTATTAAGTACTGTA-----AAAAG 383
Qy 159 shisgilygY-----ValArgphe-----SerValangl 169
Db 384 TGATGGGGGTACATATGACATATATACACTACGCTTATACGACCTTCATTTGATGG 443
Qy 169 Y-----ArgAspTYrPhegluValleuIleSerAsnAlaGlYglYal 184
Db 444 CGATCGCACTACTTTTACGACGAGTACTGAGTGTCCCAAGACAGAA-----CCAAC 497
Qy 184 aglyserIleglSerValPheIlelysglyserlysmThrglYTrpMecAlameterar 204
Db 498 CGAAGACGACGTCATACATCACTTCACGACATCATGTAAACGATGAGAGCCATGGAAT 557
Qy 204 gAsnTPglYserAsnTPglInSerAsnAlaTYrLeuAnnglyGlnSerleuSerPhear 224
Db 558 GAATCTGGGCGAGTAATTTGG-----GCTTACCA 584
Qy 224 gValThrThrThraSpglY 230
Db 585 AGTCATGGCGACAGAAAGA 603

RESULT 10
US-11-170-653-10
; Sequence 10, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibito
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-11-170-653-10

Alignment Scores:
Pred. No.: 9.73 Length: 645
Score: 89.00 Matches: 48
```



```
US-10-660-499a-2 (1-255) x US-10-660-499a-6 (1-269)
QY 185 GlySerIleGlnSerValPheIleYgLYSerIleYrThrGlyTyrMetAlaMetSerArg 204
    |||
Db 268 GGATCATCCAAATCAGTGTTCATTAAAGCTCAAAAAGTGAAGGAGTGAAGTCAAGA 209
QY 205 AenTTPGlySerAenTTPGlnSerAenAlaTyrIleuAnGlyGlnSerIleuSerPheArg 224
    |||
Db 208 AATGGGGTTCATATGGCAATCCAAATGCGTATTTGATGTCATCTTGTCTTCAGG 149
QY 225 ValThrThraSPgIyGluThraArgValPheGlnAspIleValProValSerTTPThr 244
    |||
Db 148 GTACCAACCACTAGTGAAGACCAAGGTTTCCAGATATGTTCAGTAAGTTGAGCA 89
QY 245 PheGlyGlnThraPheSerSerProValGlnPhe 255
    |||
Db 88 TTCGGCCAAACTTCTCTAGCCCAAGTTCAGTTTC 56

RESULT 5
US-10-660-499a-7
; Sequence 7, Application US/10660499A
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG-KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG-KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 389
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA probe (sense)
US-10-660-499a-7

Alignment Scores:
Pred. No.: 2,71e-31 Length: 389
Score: 380.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.08% Indels: 0
DB: Gaps: 0

US-10-660-499a-2 (1-255) x US-10-660-499a-7 (1-389)
QY 185 GlySerIleGlnSerValPheIleYgLYSerIleYrThrGlyTyrMetAlaMetSerArg 204
    |||
Db 2  GGATCATCCAAATCAGTGTTCATTAAAGCTCAAAAAGTGAAGGAGTGAAGTCAAGA 61
QY 205 AenTTPGlySerAenTTPGlnSerAenAlaTyrIleuAnGlyGlnSerIleuSerPheArg 224
    |||
Db 62  AATUGGGGUTCUAATUGGCAUCCAAATGCGUATUUGAUGUCAUCUUUUGUCUUCAG 121
QY 225 ValThrThraSPgIyGluThraArgValPheGlnAspIleValProValSerTTPThr 244
    |||
Db 122  GUACACCAACCACTAGTGAAGACCAAGGTTTCCAGATATGTTCAGTAAGTTGAGCA 181
QY 245 PheGlyGlnThraPheSerSerProValGlnPhe 255
    |||
Db 182  TTCGGCCAAACUUUCUCAAGCCCAAGTTCAGTTTC 214
```

```
RESULT 6
US-11-080-991-103
; Sequence 103, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; FILE REFERENCE: MRI-039
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; CURRENT APPLICATION NUMBER: US/11/080,991
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 2429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-103

Alignment Scores:
Pred. No.: 1.09 Length: 2429
Score: 105.00 Matches: 58
Percent Similarity: 36.28% Conservative: 24
Best Local Similarity: 25.66% Mismatches: 87
Query Match: 7.48% Indels: 58
DB: Gaps: 9

US-10-660-499a-2 (1-255) x US-11-080-991-103 (1-2429)
QY 4  IleMetIleuValIleuGlySerIleuIleGlyIleuCySAspPheThrIleThrTyrAla 23
    |||
Db 392  GTGATTCGAGTCCGTGCTATGCTCATATGATGATGATGATGATGATGATGATGATGATGAT 451
QY 24  PheSerProSerGlyTyrThrPheAlaIleAlaThrPhe----- 36
    |||
Db 452  GCCTCCACGCTTGCCCTGGGACAGAGGCTATGAACTTCCCTTTTAAAGAGTACTAGTACGC 511
QY 37  -----TyrGlyGlySerAspAlaSerGlyThrMetGlyGlyValaCySgIyTyrGlyAsn 54
    |||
Db 512  TACCTTTATGAGAGAACT--GGCTTTGATGACTAGCAAGTGGCTATGATGCTAT 568
QY 55  LeuTyrAlaThrGlyTyrGlyThrArgThr-----Ala 65
    |||
Db 569  GGTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 628
QY 66  AlaIleuSerThrAlaIleuPheAsn-----AspGlyAlaSerCysGlyGlnCysTyrLys 83
    |||
Db 629  GCCATGGCTGCTCTT-TTGTTTCATGCGCGTGGTGAATCTTGTATACAGTGTATTAAG 687
QY 84  Ile-----IleCySAspTyrIleSerAspSerArgTyrCysIleLys 97
    |||
Db 688  ATCTGAATGTCACGAACAAGAAATATCTTAACTGATATATGATGATGATGATGATGATGAT 747
QY 98  GlyArgSer----- 100
    |||
Db 748  GGGCATCATGCTGTTTATTCACCAATGCTATATATATGAGGATGAGTGAACCACTGCTCA 807
QY 101  -----ValThrValThrAlaThrAsnProProAsn---PheAlaIleuPr 116
    |||
Db 808  GTCTTCGATCTCTATATGATGCTTCAAAATATATGCTGCTGCAACCAATTTATATACACC 867
QY 116  AlaAsnAsnAsnGlyGlyTTPCySAsnProProLeuLysIlePheAspMetAlaGlnProAl 136
    |||
Db 868  TGCAGCTACTGAGCTCTAGCTGATCAGATATTTATCTACTACTGCTGCTGATGATCCCA 927
QY 136  aTTPGlyIleGlyIleTyrArgGlyIleValProValIleuPheGlnArgValPr 156
    |||
Db 928  G---GAGGCCATTTGCCATTTGCTGAGGCTTCAATATATTTGCTTTGCTTTAATA-- 982
    |||
QY 156  oCySAspIleValArgPheSerValaIleuGlyArgAspTyrPheGluIleuVal 176
```

```
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (117)..(117)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (150)..(150)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (156)..(156)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (159)..(159)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (174)..(174)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (177)..(177)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (180)..(180)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (183)..(183)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (186)..(186)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (189)..(189)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (192)..(192)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (195)..(195)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (198)..(198)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (210)..(210)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (213)..(213)
/ OTHER INFORMATION: n is a, c, g, or t.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (222)..(222)
/ OTHER INFORMATION: n is a, c, g, or t.
/
```

Alignment Scores:

```
Pred. No.: 1,31e-78 Length: 519
Score: 822.00 Matches: 143
Percent Similarity: 82.66% Conservative: 0
Best Local Similarity: 82.66% Mismatches: 30
Query Match: 58.59% Indels: 0
DB: 6 Gaps: 0
```

US-10-660-499a-2 (1-255) x US-10-660-499a-5 (1-519)

```
QY 41 AspaLaserglyThrmecGlyyAlaCyseglyTyrglyAsnleuTyraLathrglyTy 60
Db 1 GAYGCMNSNGNACNATGGNGNGCNGTGYGNTAYGNAAYTYTAYACNACNGNTAY 60
QY 61 GlyThraGthraAlaLeuSerThraAlaLeuPheAsnArglyAlaSerGlygln 80
Db 61 GGNACNMGNACNGCNGCYTWNACNGNTNTTYTAAAGAYGNGCWNSTGYGNCAR 120
QY 81 CysTyTybIleIleCyAspTyTyTySerAspSerArgTyTyGlyIleGlyArgSer 100
Db 121 TGYTAAARATATATGTGAYTAARWSNGAYWSNMGNTGTGYATHAARGGNNGNSN 180
QY 101 ValThrValThrAlaThraAsnPhcCysProPheAsnPhcAlaLeuProAsnAsnAngly 120
Db 181 GTNACNGTNACNGCNAACNAATTYTGYCCNCAATTYTGCYTTCCNAATYAAYAGSN 240
QY 121 GlyTPCyAsnProProLeuLysHsPheAspMetAlaGlnProAlaTPgIuTybIle 140
Db 241 GGNTGGTGAACCNCCNCTNNAARCAATTYTGAATGGCNCARCCNGCNGTGGARARAT 300
QY 141 GlyIleTyTyArgGlyGlyIleValProValLeuPheGlnArgValProCysLysbIle 160
Db 301 GGNATHTAYMGNGNGNATGTCNGTNTNTTYCANMGNTCCNGTGYAARARCA 360
QY 161 GlyGlyValArgPheSerValaAnglyArgAspTyTyPheGlyLeuValLeuIleSerAsn 180
Db 361 GNGGNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGT 420
QY 181 ValGlyGlyAlaGlySerIleGlnSerValPheIleGlySerIleThrglyTyPmet 200
Db 421 GTNNGNGNGCNGCNGWSNATHCARMSNGTNTTYATHAAGCWNNAARACNGTGGATG 480
QY 201 AlaMetSerArgAsnTPgIySerAsnTPgIySerAsn 213
Db 481 GCNATGWSNMGNDAATYGGGNGWSNAAATGCGCARMSNAAY 519
```

RESULT 4

```
US-10-660-499a-6/c
; Sequence 6, Application US/10660499A
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG-KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG-KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 269
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA Probe (antisense)
US-10-660-499a-6
```

Alignment Scores:

```
Pred. No.: 1.65e-31 Length: 269
Score: 380.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.08% Indels: 0
DB: 6 Gaps: 0
```

Qy	228	ThrpheSgYgUthThArgValPheInApheInIeValProValSerTriPThPheGIgIn	247
Db	601	AGTGAATGGGCGCACTCTCACTGCGCTATATCTGTTCTTCATTGGCAATTTGGCCAA	660
Qy	248	ThrpheSerSerProValGInPhe	255
Db	661	ACCTATGAAGGCCCT---CAATTC	681
RESULT 3			
US-10-660-499A-5			
Sequence 5, Application US/10660499A			
Publication No. US20050246795A1			
GENERAL INFORMATION:			
APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION			
APPLICANT: LEE, JONG SEOB			
APPLICANT: LEE, DONG-KEUN			
APPLICANT: AHN, JI HOON			
APPLICANT: SONG, SANG-KEE			
APPLICANT: CHOI, YANG DO			
TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND			
TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT			
FILE REFERENCE: 20020-020USA			
CURRENT APPLICATION NUMBER: US/10/660,499A			
PRIOR FILING DATE: 2003-09-12			
PRIOR APPLICATION NUMBER: KR 2003-19069			
PRIOR FILING DATE: 2003-03-27			
NUMBER OF SEQ ID NOS: 9			
SOFTWARE: PatentIn version 3.3			
SEQ ID NO 5			
LENGTH: 519			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Probe			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (6)..(6)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (9)..(9)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (12)..(12)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (15)..(15)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (21)..(21)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (24)..(24)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (27)..(27)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (33)..(33)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (39)..(39)			
OTHER INFORMATION: n is a, c, g, or t.			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (45)..(45)			

Score:	1403.00	Matches:	25
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-660-499A-2 (1-255) x US-10-660-499A-1 (1-1089)

QY	1	MetGlyValIleMetLeuValLeuGlySerLeuIleGlyLeuGlyCysPheThrIleThr	20
Db	52	ATGGGCAAAATATGCTGTATTTGGGTAGCTCTATTGGATTATGCTGTTCAAAATCACT	111
QY	21	ThrTyrAlaPheSerProSerGlyTyrPThrAsnAlaHisnAlaThrPheTyrGlyGlySer	40
Db	112	ACCTATGCTCTTCACTCCTCTGGATTGACCAAGCCCAATGCCACTTTTATGGGGGTAGT	171
QY	41	AspAlaSerGlyThrMetGlyGlyValaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyr	60
Db	172	GATGCTTCAGAAACTATGGGGGAGCGCTTGGGTATGGGAATCTGATGCAATCGGGTAT	231
QY	61	GlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyValaSerCysGlyGln	80
Db	232	GGAATCTAGAACTGACGACTTTAAGCACTGCTTATTTAAAGATGAGCTTCTGGGTGAG	291
QY	81	CysTyrLeuIleIleCysAspTyrLeuSerAspSerArgTyrCysIleGlyArgSer	100
Db	292	TGCTACAAATATTATATGATATTACAAATCAGACTTATGATGGTGCATCAAGGAAGATCT	351
QY	101	ValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly	120
Db	352	GTAACCGTAACGCCCAAACTTTTCCCTCCCAATTTGCCCTTCAACAAATGGA	411
QY	121	GlyTyrProCysAsnProProLeuIysHisPheAspMetAlaGlnProAlaTyrGlyValIle	140
Db	412	GCGTGGTGCACCCCACTCAAGCAATTTGATATATGAGCCCAACCCGCTGGGAAAGATT	471
QY	141	GlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysIleIysHis	160
Db	472	GGTATTATACAGAGAGGATCGTCCCGTGTCTATTCAAGGGTTCATCCAAAAAGCAT	531
QY	161	GlyGlyValaIysPheSerValAsnGlyIysAspTyrPheGlyLeuValIleuIleSerAsn	180
Db	532	GGAGGGGTTAGGTTCAGTGTGATGGAGGGAGCACTACTTGAAGCTATGATCAAGCAAT	591
QY	181	ValGlyValAlaGlySerIleGlnSerValPheIleIysGlySerIysThrGlyTyrMet	200
Db	592	GTGGGGGGGCTGGGATTCATCCAAATCAGTGTCAATTAAAGCTCAAAAATCGAGTGAATG	651
QY	201	AlaMetSerArgAsnTyrGlySerAsnTyrGlnSerAsnAlaTyrLeuAsnGlyGlnSer	220
Db	652	GCAATCTCAAGAAATTGGGGTCTTAATTGGCAATCCAAATCGATTTTGAATGGTCATCT	711
QY	221	IeuSerPheArgValThrThrAspGlyIuThrArgValPheGlnAspIleValPro	240
Db	712	TGTGCTCTCAGGGTCAACCACTGATGGAGAACCAAGATTTTCCAAAGATATTGTTCCA	771
QY	241	ValSerTyrThrPheGlyGlnThrPheSerSerProValGlnPhe	255
Db	772	GTAAGTTGACATTCGGCCAAACTTTTCTAGGCCAGTTCAAGTTC	816

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RESULT 2
US-10-670-009-1
; Sequence 1, Application US/10670009
; Publication No. US20050272041A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J.
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gultinan, Mark
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Jun, Shi
; TITLE OF INVENTION: Purified Plant Expansin Proteins and DNA Encoding Same
; FILE REFERENCE: P0466CUS08
; CURRENT APPLICATION NUMBER: US/10/670,009

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1 CURRENT FILING DATE: 2003-09-24
2 PRIOR APPLICATION NUMBER: US 09/896,301
3 PRIOR FILING DATE: 2001-06-29
4 PRIOR APPLICATION NUMBER: US 09/092,16C
5 PRIOR FILING DATE: 1998-06-05
6 PRIOR APPLICATION NUMBER: US 09/429,675/
7 PRIOR FILING DATE: 1999-10-28
8 PRIOR APPLICATION NUMBER: US 08/834,322/
9 PRIOR FILING DATE: 1997-04-15
10 PRIOR APPLICATION NUMBER: US 08/444,515/
11 PRIOR FILING DATE: 1995-05-12
12 PRIOR APPLICATION NUMBER: US 08/242,090/
13 PRIOR FILING DATE: 1994-05-12
14 PRIOR APPLICATION NUMBER: US 08/060,944/
15 PRIOR FILING DATE: 1993-05-12
16 NUMBER OF SEQ ID NOS: 13
17 SOFTWARE: PatentIn version 3.2
18 SEQ ID NO 1
19 LENGTH: 681
20 TYPE: DNA
21 ORGANISM: Cucumis sativus
22 US-10-670-009-1

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US-10-660-499A-2 (1-255) x US-10-670-009-1 (1-681)

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Percent Similarity:	80.00
Best local Similarity:	68.42
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Conservative:	15
Mismatches:	40
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QY 48 GYlaaCYsgLYrYrGylAAsnleuTYrAlaThrGylYrGylYThxArGThraaIaleu 67

Db 70 GGAGCTTGTTGGGTATGGGAATTTATACAGCCAAAGGGTATGGCAGCAACGGGGGGCTG 129

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Db 130 AGCACTGGCTATTTAACAAATGATGAAGTTGGTGGCTGGCTTCGAAATGACTTGT-- 186

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Db 187 --ACAAACGACCTTAATATGGTGGCTCCGGGA--ACTATTAAGGTGACTGCCACCAAC 240

QY 108 PheCYsPpocAspPhaAlaIeuprOAspAsnAsnGlyYrGylTYpCYsAsnPpocIeu 127

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QY 128 LysHisPheAspMetAlaGlnProAlaTrpGlyLeIeGlyYlLeTYrArGylYlLe 147

Db 301 CAACACTTCGACATGGCTGAGCGCTCGCTCTTCAATGCGCTCAATACCGACGCTGGATC 360

QY 148 ValProValIeuphGlnArGylAlaProCYsYlyHisGlyYlYlAlaArgPheSerVal 167

Db 361 GTCCCGGCTCTCTTTCGGTGGGTACCAATGATGAAAGTGGAGTGAAGGATTACATC 420

QY 168 AsnGlyArGpArYrPheGlyIuIeuValIeuIleSerAsnValGlyYlAlaGlySerIle 187

Db 421 AATGGCCACTATCTCTCAACTCGTTTGAACAAAGTGGGTGGCGAGCGCAAGTC 480

QY 188 GlnSerValPheIleYsgLYseIYsIthrGylTYpMetAlaMetSerArgAsnTrpGly 207

Db 481 CACTCTGTGTCGATTAAGGGGTCTCGAATCGATGCAATCCATGCTCTGAATTTGGGC 540

QY 208 SerAsnTrpGlnSerAsnAlaTYrIleuAsnGlyGlnSerIleuSerPheArgValIthThr 227

Db 541 CAAATCTGGCAAGCAACACTATCTCAATGGCGAAGCCCTTCTTCAAGTCACTCTT 600

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2006, 21:50:45 ; Search time 394 Seconds
(without alignments)
523.817 Million cell updates/sec

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Perfect score: 1403
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -LOCAL-ALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10660499 @CGN 1.1 184 @rnat.10012006.105622.16509
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-LONGLOG -DEV TIMEOUT=120 -MAXN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA.New:

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9: /cgcn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgcn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	100.0	1089	6	US-10-660-499A-1 Sequence 1, App11
2	889	63.4	681	6	US-10-670-009-1 Sequence 1, App11
3	822	58.6	519	6	US-10-660-499A-5 Sequence 5, App11
4	380	27.1	269	6	US-10-660-499A-6 Sequence 6, App11
5	380	27.1	389	6	US-10-660-499A-7 Sequence 7, App11
6	105	7.5	2429	7	US-11-080-991-103 Sequence 103, App
7	89.5	6.4	128978	6	US-10-775-169-345 Sequence 345, App
8	89	6.3	642	6	US-10-517-939-187 Sequence 187, App

9	89	6.3	642	6	US-10-517-939-223	Sequence 223, App
10	89	6.3	645	7	US-11-170-653-10	Sequence 10, App1
C 11	87	6.2	120096	7	US-11-121-086-24	Sequence 24, App1
C 12	86.5	6.2	8305	7	US-11-128-061-872	Sequence 872, App
C 13	86	6.1	1872	6	US-10-467-657-337	Sequence 337, App
C 14	85	6.1	1873	6	US-10-750-185-57411	Sequence 57411, A
C 15	85	6.1	1873	6	US-10-750-623-57411	Sequence 57411, A
16	84.5	6.0	2170	6	US-10-995-561-139	Sequence 139, App
17	84	6.0	1047	6	US-10-517-939-161	Sequence 161, App
18	83.5	6.0	657	7	US-11-170-653-11	Sequence 11, App1
19	83.5	6.0	2226	7	US-11-052-554A-545	Sequence 545, App
20	83.5	6.0	2366	7	US-11-136-527-22913	Sequence 22913, App
C 21	83.5	6.0	3564	6	US-10-601-368-20	Sequence 20, App1
C 22	83.5	6.0	3590	7	US-11-052-554A-520	Sequence 520, App
C 23	83.5	6.0	4858	6	US-10-601-368-19	Sequence 19, App1
C 24	83.5	6.0	191091	7	US-11-121-086-60	Sequence 60, App1
C 25	83	5.9	921	6	US-10-467-657-2791	Sequence 2791, App
C 26	83	5.9	921	6	US-10-467-657-6737	Sequence 6737, App
27	83	5.9	1065	6	US-10-517-939-215	Sequence 215, App
28	82.5	5.9	7200	7	US-11-052-554A-476	Sequence 476, App
C 29	82	5.8	2040	6	US-10-467-657-8369	Sequence 8369, App
C 30	82	5.8	2148	6	US-10-467-657-7611	Sequence 7611, App
C 31	82	5.8	4064	7	US-11-136-527-2790	Sequence 2790, App
C 32	81.5	5.8	1463	6	US-10-775-169-337	Sequence 337, App
C 33	81.5	5.8	1647	7	US-11-137-465-14	Sequence 14, App1
34	81.5	5.8	2380	7	US-11-109-157A-30	Sequence 30, App1
35	81	5.8	1401	6	US-10-517-939-275	Sequence 275, App
36	81	5.8	3024	6	US-10-517-939-83	Sequence 83, App1
C 37	80.5	5.7	1392	7	US-11-182-946-1	Sequence 1, App1
C 38	80.5	5.7	1609	6	US-10-793-626-4419	Sequence 4419, App
C 39	80.5	5.7	2462	7	US-11-136-527-4073	Sequence 4073, App
C 40	80.5	5.7	2858	6	US-10-793-626-3777	Sequence 3777, App
41	80.5	5.7	3379	6	US-10-793-626-4138	Sequence 4138, App
42	80.5	5.7	4719	6	US-10-793-626-2905	Sequence 2905, App
43	80.5	5.7	6421	6	US-10-485-517-27	Sequence 27, App1
C 44	80	5.7	1102	6	US-10-131-826A-299	Sequence 299, App
45	80	5.7	1644	7	US-11-052-554A-664	Sequence 664, App

ALIGNMENTS

RESULT 1
US-10-660-499A-1
Publication US/10660499A
GENERAL INFORMATION:
APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
APPLICANT: LEE, JONG SEOB
APPLICANT: LEE, DONG KEUN
APPLICANT: AHN, JI HOON
APPLICANT: SONG, SANG-KEE
TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
FILE REFERENCE: 20020-0205A
CURRENT APPLICATION NUMBER: US/10/660,499A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: KR 2003-19069
PRIOR FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 1089
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(816)
OTHER INFORMATION: Glycine max expansin (GmEXPI)
US-10-660-499A-1
Alignment Scores: 1.35e-140 Length: 1089
Pred. No.:

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US-10-660-499a-2 (1-255) x ADX13859 (1-1455)

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QY      20 ThrThrTyrLalPheSerProSerGlyTyrThrAsnLahiSalathPheTyrGlyGly 39
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QY      40 SerAspAlaSerGlyThrMetGlyGlyValaCysGlyTyrGlyAsnLeuTyrAlaThrGly 59
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QY      60 TyrGlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGly 79
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QY      80 GlnCysTyrLysIleIleCysAspTyrLysSerAspSerArgTyrCysIleLysGlyArg 99
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QY      100 SerValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsn 119
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QY      120 GlyGlyTyrCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaATrpgLys 139
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QY      140 IleGlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysLysLys 159
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Job time : 509 secs

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 DB 688 AGCTCTC 694
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 ACN46900;
 ACN46900;
 02-DEC-2004 (first entry)
 DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-K6-G8, SEQ:1681.
 XX Cotton; plant; EST, expressed sequence tag; transgenic plant; seed;
 KM variety DP50B; library LIB3825; molecular tag; molecular marker;
 KM genetic mapping; molecular mapping; seed germination; plant growth;
 KM plant quality; plant yield; plant breeding; tissue printing; ss.
 XX Gossypium hirsutum.
 OS US2004123340-A1.
 XX 24-JUN-2004.
 PD 12-DEC-2001; 2001US-00021323.
 PF 14-DEC-2000; 2000US-0255619P.
 PR (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
 DR WPI, 2004-479808/45.
 PT New isolated nucleic acid molecule that encodes a plant protein or its
 fragment, useful for isolating a variety of agronomically significant
 PT genes associated with plant growth, quality or yield, and as molecular
 PT tags to map genes.
 XX Claim 1; SEQ ID NO 1681; 34pp; English.
 PS The invention relates to 17880 cotton expressed sequence tags (ESTs;
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 CC from primed or non-primed seeds from variety DP50B, mature seeds from
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
 CC tissue, developing fibres, carpel walls and septa from variety
 CC Ncotton3B. The invention also relates to substantially purified
 CC proteins or their fragments encoded by nucleic acid molecules of the
 CC invention, and to transformed plants having a nucleic acid construct
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful
 CC molecular tags to isolate genetic regions, to isolate genes, to map
 CC genes, to determine gene function and to determine whether genes are
 CC members of a particular gene family. The nucleic acid molecules may be
 CC used for isolating a variety of agronomically significant genes
 CC associated with plant growth, quality, yield and could also serve as
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are
 CC also useful for identifying genes important in initiating and maintaining
 CC seed germination or that may be used to mitigate stresses encountered
 CC during seed germination. The ESTs additionally enable the acquisition of
 CC promoters and cis-regulatory elements which will be useful to express
 CC agronomically significant genes in these tissues and/or other tissues,
 CC and also permits the acquisition of molecular markers useful in breeding
 CC schemes, genetic and molecular mapping, and in cloning of agronomically
 CC significant genes. The nucleic acid molecules are further useful for
 CC detecting the expression level or pattern of a protein or mRNA and for
 CC detecting the presence or quantity of a protein by tissue printing. The
 CC present sequence represents a specifically claimed EST isolated from a

CC cotton variety DP50B primed seed cDNA library (LIB3825). The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docID=US20040123340
 XX
 SQ Sequence 576 BP; 144 A; 136 C; 144 G; 152 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8,59e-88 Length: 576
 Score: 944.00 Matches: 167
 Percent Similarity: 94.24% Conservative: 13
 Best Local Similarity: 87.43% Mismatches: 11
 Query Match: 67.28% Indels: 0
 DB: 13 Gaps: 0
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 QY 125 ProProLeuLysPheAsnAspMetAlaGlnProAlaTrpGlyLysIleGlyTrpArg 144
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 QY 185 GlySerIleGlnSerValPheIleLysGlySerLysTrpGlyTrpMetAlaMetSerArg 204
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 DB 543 TTTGGCCAGACTTTCCTTAGCAAACTACAAATTC 575
 RESULT 13
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 ID ACN46903 standard; cDNA; 601 BP.
 ACN46903;
 ACN46903;
 02-DEC-2004 (first entry)
 DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-K6-H7, SEQ:1684.
 XX Cotton; plant; EST, expressed sequence tag; transgenic plant; seed;
 KM variety DP50B; library LIB3825; molecular tag; molecular marker;
 KM genetic mapping; molecular mapping; seed germination; plant growth;
 KM plant quality; plant yield; plant breeding; tissue printing; ss.
 XX Gossypium hirsutum.

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PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
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PR 27-JUL-1999; 99US-0145293P.
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PR 27-JUL-1999; 99US-0145319P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161559P.
PR 26-OCT-1999; 99US-016160P.
PR 26-OCT-1999; 99US-0161616P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.
```

Alignment Scores:

Pred. No.:	2,2e-89	Length:	695
Score:	960.50	Matches:	174
Percent Similarity:	86.55%	Conservative:	19
Best Local Similarity:	78.03%	Mismatches:	26
Query Match:	68.46%	Indels:	4
DB:	3	Gaps:	1

US-10-660-499a-2 (1-255) x AAC41531 (1-695)

```
QY 3 LysIleMetLeuValIleuGlySerLeuIleGlyLeuCysGlyPheThr-----Ile 19
DB 28 AAAGTCATATCATCAAGTCTTCTAGCTGATGGCGGTTTGGCCGCTCTTTTATT 87
QY 20 ThrThrTyraAlaPheSerProSerGlyTyrPThrAsnAlaHisAlaThrPheTyrgly 39
DB 88 GCTGTTGATGCGTTTAAGCTTGTGTTTAACATAATGGCCACGACCTACATTCATGAGGA 147
QY 40 SeraspAlaSerGlyThrMet-GlyGlyAlaCysGlyTyrglyAsnLeuTyraIaThrGly 59
DB 148 AGTGAAGCTTCTGGAAACATGGGGTGGAGCTTGTGGTACGGAGATCTTACTCGGCGGG 207
QY 59 TyTyrglyThrArgThrAlaAlaIleuSerThrAlaIleuPheAsnAspGlyAlaSerCysGly 79
DB 208 GTACGGGACAATGACCGGACCGTTTACGACCGGCTGTTTCAACGAGGAGCTTTCGGG 267
QY 79 yGlnCytyrTyrsIleIleCysAspTyrylYssSerAspSerArgTyrCyGiletyGlyAr 99
DB 268 AGAATGCTATAGATTAACGTGTGATCAGCGGCGGACTCACGGTGTGCTTGAAAGGACG 327
QY 99 gSerValThrValThrAlaThrAsnPheCysProProAsnPheAlaIleuProAsnAsnAs 119
DB 328 TTCTGTGTATTATACAGCCACTTACTTTGGCCACCAACTTGTGCTTACCAACAACA 387
QY 119 ngIyGlyTyrPcyAsnProProIleuTyrsIlePheAspMetAlaIleuProAlaTyrGly 139
DB 388 CGGTGGTGTGTGCAATCCGCGCTTAACATTTCCAGATGGCAACCCGCTGGGAAAA 447
QY 139 sIleGlyIleTyraTyrglyGlyIleValProValIleuPheGlnArgValProCyAsyBy 159
DB 448 GATCGGAATTTACAGGAGGAGGATCGTCCCGCTTTCCAAAGAGTGAGCGTTACAA 507
QY 159 sHsIyGlyValArgPheSerValAsnGlyArgAspTyrrPheGluIleuValIleuIese 179
DB 508 GAAAGGAGAGTTAGATTCAAGATTAAACGGAGAGACTTCTGACCTAGTGAACATTCA 567
QY 179 rAsnValIyGlyAlaGlySerIleGlnSerValPheIletyGlySerIySerThyGlyTyr 199
DB 568 AATGTAGAGGAGGAGGTTCTATTAACTGTATCATCAAGATCAAAAGATCAAGAGCTGGT 627
QY 199 pMetAlaMetSerArgAsnTyrGlySerAsnTyrGlnSerAsnAlaTyIleuAsnGly 219
```


CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactamman,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 1053 BP; 180 A; 336 C; 315 G; 222 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,52e-97	Length:	1053
Score:	1042.00	Matches:	186
Percent Similarity:	84.68%	Conservative:	24
Best Local Similarity:	75.00%	Mismatches:	38
Query Match:	74.27%	Indels:	0
DB:	13	Gaps:	0

US-10-660-499a-2 (1-255) x ADX54060 (1-1053)

QY 8 leuGlySerIleuIleGlyLeuCySPhethrThIethrThrYalApheserProser 27
DB 116 CTTCGCTTGTCTTGGCGGCTCTTCTGGAAGAGACCCGCGCTTCTGCGCTC 175
QY 28 GYTrpThrAsnAlaHisAlaThrPheYrGlyYrGlySerAspAlaSerGlyYrHmeGly 47
DB 176 GGGCTAAACAAGCGCTTCCGACCTTCTATGGCGGTAGCAGCCCTTACGAAAGATGGGT 235
QY 48 GYAlaCYeGlyYrYrGlyAsnLeuYrYrAlaThrGlyYrGlyYrThrArgThrAlaAlaLeu 67
DB 236 GGGGCTGTGGGTAGACCGCAACCTGTACTGACCGGGTACCGCACCGACGGCGGCGT 295
QY 68 SerThrAlaIleuPheAsnAspGlyAlaSerCyGlyGlnCySerYrYrIleleCYeAsp 87
DB 296 AGACGCGGCTTCAACGACGCGGCTCTGTGGGAGAGTCAACCGGATCCCTGCGAC 355
QY 88 YrYrYSerAspSerArgTrpCySileYrGlyArgSerAlaThrYrAlaThrAsn 107
DB 356 TACCAAGCGGACCCGCGGCTTCTGCTCCGCGACGCTGTCACATCCGCAACCGCACAC 415
QY 108 PheCyProProAsnPheAlaIleuProAsnAsnGlyYrYrCyAsnProProLeu 127
DB 416 CTGTGCGCTCCCAACTACGCGCTGCCAAGACGACGCGGCTGTGTCACCCGCGCGG 475
QY 128 YrHisPheAspMetAlaGlnProAlaTrpGlnYrIleGlyYrIleYrArgGlyYrIle 147
DB 476 CAGCACTTCAACATGCGCGGCTGCTCAAGATCGGATCAACCGCGCGGCTC 535
QY 148 ValProValIleuPheGlnArgValProCyYrYrIleGlyYrValArgPheSerVal 167
DB 536 GTGCCGCTCAACTACCAAGAGGTGCGGTGTGTAAGAAAGCGGGTGAAGCTTCAAGCATC 595
QY 168 AsnGlyArgAspYrPheGlnLeuValIleuIleSerAsnValGlyYrAlaGlySerIle 187
DB 596 AAGCGGCGGACACTTCACTGAGTGTCTCATCTCAAGCTGGGCGGCTGCGGTCCATC 655
QY 188 GlnSerValPheIleYrGlySerYrYrThrGlyYrPheAlaMetSerArgAsnTrpGly 207
DB 656 CAGTCCGCGCTCAATCAAGGGGTGCGCACCGGGTGAATGCCATGTCCCGAACTGGGCG 715
QY 208 SerAsnTrpGlnSerAsnAlaYrYrLeuAsnGlyYrSerIleSerPheArgValThrTrp 227
DB 716 GTCACTGGGAGTCAACGCGTACTCAATGGCAGAGCTGTGCTTCAAGTCAACAGC 775
QY 228 ThrAspGlyYrGlnThrArgValPheGlnAspIleValProValSerTrpThrPheGlyGln 247
DB 776 AGGAGGCGGACAGCAAAACCTTCCCGAGTGTGCGCGCCGCAAGCTTGGGGGTTCGGTCA 835
QY 248 ThrPheSerSerProValGlnPhe 255

DB 836 ACCTTTCGACCTCGCAGCAGTTC 859

RESULT 10

ADa69924
ID ADa69924 standard; DNA; 789 BP.

XX
AC ADa69924;

XX
DT 20-NOV-2003 (first entry)

XX
DE Rice gene, SEQ ID 3247.

XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.

XX
OS Oryza sativa.

XX
PN MO2003000898-A1.

XX
PD 03-JUN-2003.

XX
PF 22-JUN-2001; 2001MO-IB001105.

XX
PR 22-JUN-2001; 2001MO-IB001105.

XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
PI Chang H, Chen W, Cooper B, Glazedbrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX
DR WPI, 2003-175290/17.

XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

XX
PS Claim 6; SEQ ID NO 3247; 899bp; English.

XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX
SQ Sequence 789 BP; 130 A; 270 C; 273 G; 116 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,92e-90	Length:	789
Score:	971.50 <td>Matches:</td> <td>168</td>	Matches:	168
Percent Similarity:	84.62% <td>Conservative:</td> <td>30</td>	Conservative:	30
Best Local Similarity:	71.79% <td>Mismatches:</td> <td>35</td>	Mismatches:	35
Query Match:	69.24% <td>Indels:</td> <td>1</td>	Indels:	1
DB:	8	Gaps:	1

US-10-660-499a-2 (1-255) x ADa69924 (1-789)

QY 23 AlaPheSerProSerGlyYrTrpThrAsnAlaHisAlaThrPheYrGlyYrGlySerAspAla 42
DB 82 GCGCTGAGACCGACGCGGTGTGGAGGCGGACGCACTTCTACGCGCGGCGGACGCG 141
QY 43 SerGlyYrHmeGlyYrAlaCYeGlyYrYrGlyAsnLeuYrYrAlaThrGlyYrGlyYr 62
DB 142 TCGGAACCATGGGCGGCGGTGTGGGTACGCAACTGTACGCGGAGGGTACGCGACG 201
QY 63 ArgThrAlaAlaIleuSerThrAlaIleuPheAsnAspGlyAlaSerCyGlyGlnCyYr 82
DB 202 AGGACGCGGCGCTCAGCAGCGGCGCTTCAACGACGCGCTGCGCGGCGAGTGTAC 261

PT New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

PS Claim 1; SEQ ID NO 17012; 15pp; English.

CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC [ftp://seeddata.uspo.gov/sequence.html?DocId:2004034888](http://seeddata.uspo.gov/sequence.html?DocId:2004034888). The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactosemannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

Sequence 1029 BP; 182 A; 330 C; 304 G; 213 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-97	Length:	1029
Score:	1043.00	Matches:	186
Percent Similarity:	84.68%	Conservative:	24
Best Local Similarity:	75.00%	Mismatches:	38
Query Match:	74.34%	Indels:	0
DB:	13	Gaps:	0

US-10-660-499A-2 (1-255) X ADX34192 (1-1029)

QY	8	LeuGIySerLeuIIleGIyLeuCyCySphenThIIleThrThrYrAlaAPheserProSer	27
		:::	
Db	99	CTTGCGTTCCTCTTGCGCGCGTCCCTTCTCTGGAAGGAACCGCGTCTCTTGCGCGTCC	158
QY	28	GIYTrpThraAsnAlaHisAlaThrPheTYrGIyGIySerAspAlaSerGIyThrMetGIy	47
Db	159	GGGCTAAACAAGCGCTTCCCACTTCTAATGGCGTAAAGCAACGCTTCAGAAAGATGGT	218
QY	48	GIYAlaCySGIYTYrGIyAsnLeuTYrAlaThnGIYTYrGIYThraGThraAlaAlaLeu	67
Db	219	GGGGCGCTGGGGTACCGCAACCTGTACTCAGCGGGTACCGCAACGACACGGCGCGCTG	278
QY	68	SeTrThraAlaLeuPheAsnAspGIyAlaSerCySGIyGInCySyrTrIySIIleIleCyAsp	87
Db	279	ACACACGGCGCTCTTCAACAACAGCGCGCTCTGCGGGCAAGTCACCGGACTCTCTGGAC	338
QY	88	TYrIySerAspSerArGIrTpCySIIleIySGIyArgSerValThraValThraAlaThraSn	107
Db	339	TTCCAGGCGGACCGCGGGTTCGATCTCCGGGCAACGTCGTGAACATCACCGGCACCAAC	398
QY	108	PheCySProProAsnPheAlaLeuProAsnAsnAmnIyGIYTrpCySAsnProProLeu	127
Db	399	CTGTGCGCTCCCACTACACGCGCTGCCCAACGACAGACCGCGCGTGTGCACACCGCGCGG	458
QY	128	IyShIaPheAspMetaIaGInProAlaTrpGIuIySIIleGIyIIleTYrArGIyGIyIIle	147
Db	459	CAGCACTTGAGACATGGCCAGCGCGGCTGAGCTCAAGATTCGACATCAACCGCGCGGATC	518
QY	148	ValProValLeuPheGInArGIyValProCySIIleIyShIaSGIyGIyValArgPheSerVal	167
Db	519	GTGCCCGTCACTACCAAGGCGTCCGTGTGTAAAGAAAGCGGGGTGAAGTTCAAGATC	578
QY	168	AAnGIyArXaAspTYrPheGIuLeuValLeuIIleSerAsnValGIyAlaIaGIySerIIle	187
Db	579	AACGGCGGACACTTCAGCTCGAGCTGCTCATCTCCAAAGTGGCGCGCTCGGGTTCATC	638

Oy	188	GlnSerValPheIleValGlySerIysThrGlyTyrPheAlaMetSerArgAntPGly	207
Db	639	CAGTCGGCGTCGATCAAGGGATCGGGACCGGGGTGATGGCCATGTCGCCGAATGGGC	698
Oy	208	SerAntTPGInSerAsnAlaTyrIleuAnGlyGlnSerIeuSerPheArgValThr	227
Db	699	GTCAACTGGAGTCCAGCGGACTCATGGCCAGAGCGTGTGTTCCAGGTCAACAGC	758
Oy	228	ThrAspGlyGluThrArgValPheGlnAspIleValProValSerTyrPheGlyGln	247
Db	759	AGCGACGGCCAGACCAAAACCTTCCCGACAGTGGCGGCCGACGCGGGGTTGGTCAG	818
Oy	248	ThrPheSerSerProValGlnPhe	255
Db	819	ACGTTTGCACCTCGCAGCAGTTTC	842
RESULT 9			
ID	ADX54060	standard; cDNA; 1053 BP.	
AC	ADX54060;		
DT	21-APR-2005	(first entry)	
DE	Plant full length insert polynucleotide seqid 28800.		
KW	plant protectant; plant growth regulant; gene therapy; plant;		
KW	recombinant DNA construct; physical array; plant breeding marker;		
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;		
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;		
KW	growth rate; cell cycle pathway; disease resistance;		
KW	galactomannan production; lignin production; plant growth regulator;		
KW	yield; plant growth; plant development; seed oil; protein yield;		
KW	protein content; gene; ss.		
OS	Unidentified.		
XX			
PN	US2004034888-A1.		
XX			
PD	19-FEB-2004.		
XX			
PF	28-APR-2003; 2003US-00425114.		
XX			
PR	06-MAY-1999; 98US-00304517.		
XX			
PR	05-NOV-2001; 2001US-00985678.		
XX			
PA	(LIU//) LIU J.		
PA	(ZHOU//) ZHOU Y.		
PA	(KOVALIC//) KOVALIC D K.		
PA	(SCRE//) SCREEN S B.		
PA	(TAB//) TABASKA J E.		
PA	(CAOY//) CAO Y.		
XX			
PI	Liu J, Zhou Y, Kovalic DK, Screen SB, Tabaska JE, Cao Y;		
XX			
DR	WPI; 2004-180133/17.		
XX			
PT	New recombinant DNA construct, useful for improving plant tolerance to		
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or		
PT	pests, for conferring increased resistance to plant diseases, or for		
PT	improving yield.		
XX			
PS	Claim 1; SEQ ID NO 28800; 15pp; English.		
XX			
CC	The invention describes a recombinant DNA construct comprising a		
CC	polynucleotide consisting of a sequence encoding an amino acid sequence		
CC	available in electronic form from the US patent office at		
CC	ftp://sedate.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide		
CC	of the invention also is useful in physical arrays of molecules and as		
CC	plant breeding markers. The recombinant DNA construct is useful for		
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme		
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in		


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PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-015138P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-015559P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. No.: 7.63e-99      Length: 1132
Score: 1055.00          Matches: 196
Percent Similarity: 79.14%      Conservative: 24
Best Local Similarity: 70.50%    Mismatches: 33
Query Match: 75.20%            Indels: 26
DB: 3                      Gaps: 2

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US-10-660-499a-2 (1-255) x AAC38981 (1-1132)

```

QY 3 LysIleMetLeuValLeuGlySerLeuIleGlyLeuCyScySphenTr-----Ile 19
DB 24 AAGTCTATATCAATGCTCAAGTCTGATTCGCGGCTTTGGCGCTCTTTTATT 83
QY 20 ThrThrTyrAlaPheSerProSerGlyTyrThrAsnAlaHisAlaThrPheTyrGlyGly 39
DB 84 GCTGTTGATGCGTTAAAGCTTCCTGTTTAACTAATGACCGCATCTATATGAGGA 143
QY 40 SerAspAlaSerGlyThrMet----- 46

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DB 144 AGTGAAGCTTCTGAAACAT-GGTAATTTCACATTAGTTCTTTATGTTGACATC 202
QY 47 -----GlyGlyAlaCyGlyTyrGlyAsnLeuTyrAla 57
DB 203 TAAATCTTAATTTCTTTGTTTTCAGGTGAGCTTGAGGATGACGATCTTACTCG 262
QY 58 ThrGlyTyrGlyThrArgThrAlaAlaSerThrAlaLeuPheAsnAspGlyAlaSer 77
DB 263 GCGGGGTACGGACATGACGCGGCTTAACAGCGCTCTGTTCAACACGAGGCTTCT 322
QY 78 CyGlyGlnCyTyrIleIleCyAsnProIleCyAsnProIleCyAsnProIleCy 97
DB 323 TCGGAGATGCTTAAGATTAACGTGTATCAAGCGGCGGCTTCAAGCGGCTTGA 382
QY 98 GlyArgSerValThrValThrAlaThrAsnPheCyProProAsnPheAlaLeuPro 117
DB 383 GAGGCTTCTGAGTTATTCAGCCACTAATTTTCCCAACCTTCTTCTTCTTCTTAC 442
QY 118 AsnAsnGlyGlyTyrCyAsnProIleuLysHisPheAspMetAlaGlnProAlaTyr 137
DB 443 AACAAAGGTGTTGGTGAATCGCGCTTAACATTCGATGACCAACCCGCTTG 502
QY 138 GluIleIleGlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCy 157
DB 503 GAAAGATCGGAATTTACAGAGAGGAATCGTCCGCTGTTTCCAAAGAGTGA 562
QY 158 LysIleHisGlyGlyValArgPheSerValAsnGlyArgAspTyrPheGluLeuVal 177
DB 563 TCAACAAAGAGGAGATTTGATTCAAGATTAACGGAGAGACTTCTCAGCTAGTGAAC 622
QY 178 IleSerAsnValGlyGlyValIleGlySerIleGlnSerValPheIleGlySerLys 197
DB 623 ATTCAAATGATGAGAGAGAGGCTTATTAATCTGTATCCATCAAGATTAAGACT 682
QY 198 GlyTyrMetAlaMetSerArgAsnTyrGlySerAsnTyrGlnSerAsnAlaTyrLeuAsn 217
DB 683 GGTGGTTAGCCATGCTCTGTAATTCGAGAGCTAATTCGATTCGATTCATGAT 742
QY 218 GlnGlnSerLeuSerPheArgValThrThrAspGlyGluThrArgValPheGlnAsp 237
DB 743 GGTCAAGCTCTCTCTTCTCTATTAACACTAATGATGATGATGATGATGATGAT 802
QY 238 IleValProValSerTyrPheGlyGlnThrPheSerProValGlnPhe 255
DB 803 GTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 856

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RESULT 7
ADK51829 standard, cDNA, 1010 BP.

ADK51829;
21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 26569.

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomanan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.

Unidentified.

US2004034888-A1.

19-FEB-2004.

28-APR-2003; 2003US-00425114.

QY 160 HisGlyValArgPheSerValaenglyArgAspTyrPheGluLeuValLeuIleSer 179
 DB 511 AAGAGGAGGATGATGATGAGAAACGGAGAGACTACTTCAAGCTAGTGAACATTCA 570
 QY 180 AasnValGlyValaGlySerIleGlnSerValPheIleGlySerIleThrGlyTyr 199
 DB 571 AATGTGGAGAGACAGATCTTATTAATCTGTATCCATCAAGATCAAGACTGGTTGG 630
 QY 200 MetAlaMetSerArgAsnTyrGlySerAsnTyrGlnSerAsnAlaTyrLeuAenglyGln 219
 DB 631 TTAGCATGTCTGTATGTTGGAGGCTAATGGCAATCGAATGCTTATCTAGATGTCA 690
 QY 220 SerLeuSerPheArgValThrThrAspGlyGluThrArgValPheGlnSepIleVal 239
 DB 691 GCTCTCTCTTCTCTATTAACACTGATGATGCTGCTACTAGACTCTTCCATGTGTGT 750
 QY 240 ProValSerThrPheArgPheGlyGlnThrPheSerProValGlnPhe 255
 DB 751 CCTTCTTCTTGTCTTGTGACAGATTATTTCCACGTCAGTTT 798
 RESULT 5
 ID ADN74396 standard; cDNA; 759 BP.
 AC ADN74396;
 XX 15-JUL-2004 (first entry)
 DT Thale cress cDNA repressed in E2Fa/Dpa expressing plants SegID 2291.
 XX gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
 KM growth regulator; animal feed product; thale cress;
 KM cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
 OS Arabidopsis thaliana.
 OS WO2004035798-A2.
 PN 29-APR-2004.
 PD 20-OCT-2003; 2003MO-EP011658.
 PF 18-OCT-2002; 2002BP-00079408.
 PR (CROP-) CROPDESIGN NV.
 PA Inze D, De Veylder L, Vlieghe K;
 PI WPI; 2004-348466/32.
 PI P-PSDB; ADN74397.
 DR Altering plant characteristics, useful for producing plants for enzyme or
 XX pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX Claim 1; SEQ ID NO 2291; 134bp; English.
 PS This invention relates to a novel method for altering one or more plant
 XX characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a

CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polynucleotide sequence is the E2Fa/Dpa
 CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa
 CC transcription factor, given in an exemplification of the invention.
 XX
 SQ Sequence 759 BP; 187 A; 153 C; 194 G; 225 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.5e-103 Length: 759
 Score: 1091.00 Matches: 195
 Percent Similarity: 86.69% Conservative: 20
 Best Local Similarity: 78.63% Mismatches: 33
 Query Match: 77.76% Indels: 0
 DB: 12 Gaps: 0
 US-10-660-499a-2 (1-255) x ADN74396 (1-759)
 QY 8 LeuGlySerLeuIleGlyLeuCysCysPheThrIleThrThrTyrAlaPheSerProSer 27
 DB 13 CTAGCTGAGTGGCGGTTTGGCCGCTCTTTTATTTGCGGTGATGCGTTTAGCCCTTCT 72
 QY 28 GlyTyrThrAsnAlaHisAlaThrPheTyrGlyGlySerAspAlaSerGlyThrMetGly 47
 DB 73 GGTTAACCTAATGCTACGCTCACTTCTATGAGAGAGTACGCTTCTGAAACAATGGCT 132
 QY 48 GlyAlaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyrGlyThrArgThrAlaLeu 67
 DB 133 GGAGCTTGTGTGTTACGAGATCTTACTCGCGGGGTACGGGCAATGACGGCGGCTTA 192
 QY 68 SerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrTyrIleCysAsp 87
 DB 193 ACACGCGCTCTGTCAACACGAGCTTCTTGCGAGAAATGCTAATGAGATACGCTGAT 252
 QY 88 TyrLeuSerAspSerArgTyrCysIleLeuGlyArgSerValThrAlaThrAsn 107
 DB 253 CACGCGCGGACTCAGCTGCTGCTTGAAGAAGCTTCTGTGTTATTCACGCACTAAC 312
 QY 108 PheCysProPheAsnPheAlaLeuProAsnAsnGlyGlyTyrCysAsnProPheLeu 127
 DB 313 TTTTGGCCACCAACTTCTTGTGCTTACCAACAACGATGTGTGCAATCGCGCTT 372
 QY 128 TyrHisPheAspMetAlaGlnProAlaTyrGlyLeuGlyTyrIleTyrArgGlyGlyIle 147
 DB 373 AAACATTTGACATGTCACACACCCGCTTGGAAMAATGGAATTTTACAGAGAGGAATC 432
 QY 148 ValProValLeuPheGlnArgValProCysLeuTyrHisGlyValArgPheSerVal 167
 DB 433 GTTCCCGTGTGTTCCAAAGAGTACGCTTACAGAAAGAGAGATTGATTCAAGTA 492
 QY 168 AenglyArgAspTyrPheGluLeuValLeuIleSerAsnValGlyValaGlySerIle 187
 DB 493 AACGGAAGAGACTACTTCAAGCTAGTGAATATTCAAAATGTAGAGAGAGAGCTTCATT 552
 QY 188 GlnSerValPheIleGlySerIleThrGlyTyrPheMetAlaMetSerArgAsnTyrGly 207
 DB 553 AATCTGTATTCATCAAGAGATCAAGACTGTTGTTGACCATGCTCTGTAATCTGGGA 612
 QY 208 SerAsnTyrGlnSerAsnAlaTyrLeuAenglyGlnSerLeuSerPheArgValThrThr 227
 DB 613 GCTAATTTGGCAATCGAATGCTTATCTAGAGTCAAGCTCTCTTTCATTCATTAACCT 672
 QY 228 ThrAspGlyGluThrArgValPheGlnAspIleValProValSerThrThrPheGlyGln 247
 DB 673 ACTGATGGTCTTACTAGAGCTTCTTCCATGTTGTTCTTCTTGTGCTTTTGAACAG 732
 QY 248 ThrPheSerSerProValGlnPhe 255
 DB 733 ATTATTTCTTCAACGTTCAAGTTT 756
 RESULT 6
 ID AAC38981 standard; DNA; 1132 BP.

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PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147436P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.

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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160811P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161040P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. No.: 2.03e-103
Score: 1098.50
Percent Similarity: 86.33%
Best Local Similarity: 76.95%
Query Match: 78.30%
DB: 3
Gaps: 1

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US-10-660-499a-2 (1-255) x AAC41263 (1-980)

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QY 3 LysIleMetLeuValLeuGlySerLeuIleGlyLeuCyCysPheThr-----Ile 19
DB 31 AAGTCATATCATCTGCAAGTCTCTAGCTGATGGCCGCTTTGGCCGCTTTATT 90
QY 20 ThrThrTyralAphSerProSerGlyTTPThAsnAlaHisAlaThrPheTyrgly 39
DB 91 GCTGTGATGCGTTTAAAGCTTCTGCTTTAACTAAATGCCACGCTTCACTTAATGAGGA 150
QY 40 SerAspAlaSerGlyThrMetGlyAlaCyGlyTyrglyAsnLeuTyralArhrgly 59
DB 151 AGTGAACGCTTTCGAAACATGGGTGAGCTGTGTGAGGATCTTTAACTGCGGCGG 210
QY 60 TyrglyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCygly 79
DB 211 TACGGGACATGACGGCAGCGTTAAGCAGCGCTCTGTTCAACGACGAGCTTCTCGGA 270
QY 80 GlnCysTyrllyIlelleCysAspTyrllySerAspSerArgTTPCysIleLysGlyArg 99
DB 271 GAATGCTATAGATTAACGTGTATCAACGGCGGAGCTCAACGGGTGCTTGAAGAGAGCT 330
QY 100 SerValThrValThrAlaThrAsnPheCyProProAsnPheAlaLeuProAsnAsn 119
DB 331 TCTGTGTTATTTACGCCACTTAAGCTTTCGCCACCAAACTTGTGCTTAACAACAAC 390
QY 120 GlyIlyTTPCyAsnProProLeuLysHisPheAspMetAlaGlnProAlaTTPGlyLys 139
DB 391 GGTGGTTGGTGCATCGCCGCTTAAACATTTGCATATGGCAACACCCCTTGGGAAAG 450
QY 140 IleGlyIleTyralArgIlyGlyIlyLeValProValLeuPheGlnArgValProCysLys 159
DB 451 ATCGGAATTTACAGAGAGGAATCGTTCCTGCTTTCCAAAGATGAGCTGTACAG 510

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PR	23-MAY-1999	99US-01265788P
PR	25-MAY-1999	99US-01265646P
PR	25-MAY-1999	99US-01267855P
PR	01-APR-1999	99US-01282632P
PR	06-APR-1999	99US-01287534P
PR	08-APR-1999	99US-01287833P
PR	15-APR-1999	99US-01298645P
PR	19-APR-1999	99US-01300777P
PR	21-APR-1999	99US-0130449P
PR	23-APR-1999	99US-01305101P
PR	28-APR-1999	99US-01308691P
PR	28-APR-1999	99US-0131449P
PR	30-APR-1999	99US-01320248P
PR	04-MAY-1999	99US-01328407P
PR	04-MAY-1999	99US-01328484P
PR	05-MAY-1999	99US-01328485P
PR	06-MAY-1999	99US-01328486P
PR	06-MAY-1999	99US-0132867P
PR	07-MAY-1999	99US-0134256P
PR	11-MAY-1999	99US-0134256P
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PR	14-MAY-1999	99US-0134218P
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PR	25-MAY-1999	99US-0136021P
PR	27-MAY-1999	99US-0136392P
PR	28-MAY-1999	99US-0136392P
PR	01-JUN-1999	99US-01372222P
PR	03-JUN-1999	99US-01375288P
PR	04-JUN-1999	99US-01375020P
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PR	10-JUN-1999	99US-01388474P
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PR	18-JUN-1999	99US-01394652P
PR	18-JUN-1999	99US-01394558P
PR	18-JUN-1999	99US-01394621P
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PR	21-JUN-1999	99US-01398177P
PR	23-JUN-1999	99US-01398699P
PR	23-JUN-1999	99US-0140353P
PR	23-JUN-1999	99US-0140354P
PR	24-JUN-1999	99US-0140683P
PR	24-JUN-1999	99US-0140823P
PR	29-JUN-1999	99US-0140991P
PR	29-JUN-1999	99US-0141287P
PR	01-JUL-1999	99US-0141642P
PR	01-JUL-1999	99US-0142154P
PR	02-JUL-1999	99US-0142055P
PR	06-JUL-1999	99US-0142230P
PR	08-JUL-1999	99US-0142803P
PR	09-JUL-1999	99US-0142920P
PR	12-JUL-1999	99US-01442977P
PR	13-JUL-1999	99US-0143542P
PR	14-JUL-1999	99US-0143624P
PR	15-JUL-1999	99US-0144005P

CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX
 XX
 SQ Sequence 1134 BP; 322 A; 244 C; 234 G; 334 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,43e-134 Length: 1134
 Score: 1399.00 Matches: 254
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 1
 Query Match: 99.71% Indels: 0
 DB: 13 Gaps: 0

US-10-660-499a-2 (1-255) x ADX27747 (1-1134)

QY 1 MetGlyValIleMetLeuValLeuGlySerLeuIleGlyLeuGlyCysPheThrIleThr 20
 DB 161 ATGGCGAATATCATGCTTGTGTTGGTACCTCATTGATTCGTTTCACATCACT 220
 QY 21 ThrTyralaPheSerProSerGlyTyPThrAsnAlaHisAlaThrPheTyrglySer 40
 DB 221 ACCTATGCTTCTCACCCTCTGATGGAACCAATGCCAATGCCACTTTTATGGGGTATG 280
 QY 41 AAPAlaSerGlyThMetGlyValaCysGlyTyrglyAsnLeuTyralaThrGlyTy 60
 DB 281 GATGCTTCAGGAACCTATGGGGGAGCTGTGTATGGGAATCTATGCAACTGGGAT 340
 QY 61 GlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGln 80
 DB 341 GGAAGTACAGCTGACCTTATGACCTGCTTATTTAATGATGAGCTTCCTGTGTCA 400
 QY 81 CysTyValIleIleCysAspTyrlsSerAspSerArgTyPcysIleGlyArgSer 100
 DB 401 TGTCTCAAAATTTATATGATTCATTCATCAATCAGACTCAGATGCGATCAAGAAATCT 460
 QY 101 ValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 120
 DB 461 GTAAACCGTAACTGCCCAAACTTTGCTCCCTCCCAATTTGCGCTTCTTAAACAATGGA 520
 QY 121 GlyTyPcysAsnProProleuGlyHisPheAsnMetAlaGlnProAlaTyPglySile 140
 DB 521 GGTGTGTGCAACCCACCTCAAGCAATTTGATATGCCCCCAACCCGCTGGGAAAGATT 580
 QY 141 GlyIleTyArgGlyGlyIleValaProValLeuPheGlnArgValaProCysIleGlyHis 160
 DB 581 GGTATTTACAGAGAGAGAGATCGCCCCGTCATTTTCAAAAGGTTTCATGCAAAAAGCAT 640
 QY 161 GlyIleValaArgPheSerValaGlnGlyArgAspTyPheGlnLeuValLeuIleSerAsn 180
 DB 641 GGAGGGGGTTAGGTTCAGTGTAATGGAGGACTACTTTGAGCTAGTATGATCAACAAT 700
 QY 181 ValGlyValaGlySerIleGlnSerValaPheIleGlySerIleGlyTyPmet 200
 DB 701 GTGGGGGGGTGCTGATTCATTCATCAGTTCATTAAAGGCTCAAAAACCTGATGATG 760
 QY 201 AlaMetSerArgAsnTyPglySerAsnTyPGLnSerAsnAlaTyrlsLeuGlnGlySer 220
 DB 761 GCAATGTCAAGAAATTTGGGTTCTAATTTGGCAATTCAAATGCGATTTGATGATCT 820
 QY 221 LeuSerPheArgValaThrThrAspGlyGluThrArgValaPheGlnAspIleValaPro 240
 DB 821 TTGTCTCTTCAAGGCTCAACCACTGATGAGAGACAGATTTCACAAATATTTGTTCA 880
 QY 241 ValSerTyPThrPheGlyGlnThrPheSerSerProValGlnPhe 255
 DB 881 GCAAGTTGACATTCGGCCAAACTTCTCTAGCCCAAGTTCAGTTTC 925

RESULT 3
 AAD03712
 ID AAD03712 standard; cDNA; 1103 BP.

AC AAD03712;

DT 19-JUN-2001 (first entry)

DE Tomato seed expansin, LeExp8, cDNA for controlling seed germination.

KM Tomato; endo-beta-mannanase; Lycopersicon esculentum mannanase2; LeMAN2;

KM polygalacturonase; PG; LexP4; cellulase; arabinosidase; LeAra; LeEXP8;

KM xyloglucan endotransglycosylase; XET; LexET4; expansin; LeEXP4; LeEXP8;

KM LeEXP10; hydrolase; endosperm cap; tissue weakening; radicle growth;

OS seed germination; ss.

XX Lycopersicon esculentum.

XX Key Location/Qualifiers

XX CDS 39..812

XX FT /tag= a

XX FT /product= "Tomato seed expansin, LeExp8"

XX PN MO200123530-A1.

XX PD 05-APR-2001.

XX PF 29-SEP-2000; 2000MO-US026884.

XX PR 30-SEP-1999; 99US-00410191.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Bradford KJ, Chen F, Dahal P, Downie B, Nonogaki H;

XX DR WPI; 2001-266144/27.

XX DR P-PSDB; AAE00413.

XX PT Novel nucleic acid sequences isolated from germinating seeds encoding

XX PT polypeptides that are useful to control seed germination in plants.

XX PS Claim 4; Page 49; 63pp; English.

XX CC The present invention relates to enzymes such as seed-specific endo-beta-

XX CC mannanase (e.g., Lycopersicon esculentum (Le) MAN2), polygalacturonase

XX CC (PG) (e.g., LexPG1), cellulases such as Cel55 and Cel68, arabinosidase

XX CC (e.g., LeAra), xyloglucan endotransglycosylases (XET) (e.g., LexET4) and

XX CC expansins such as LexKP4, LeEXP8 and LeEXP10 isolated from germinating

XX CC seeds. All these enzymes are expressed initially in the endosperm caps

XX CC and are associated with cell wall hydrolysis. These enzymes are

XX CC associated with weakening of tissues surrounding the embryo and/or

XX CC initiating radicle growth. The control of expression of these endogenous

XX CC genes is therefore a convenient means for controlling seed germination.

XX CC The present sequence is tomato seed expansin, LeExp8, cDNA. Expansins are

XX CC extracellular proteins that facilitate cell wall extension

SQ Sequence 1103 BP; 370 A; 158 C; 227 G; 348 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-104 Length: 1103
 Score: 1110.50 Matches: 195
 Percent Similarity: 88.14% Conservative: 28
 Best Local Similarity: 77.08% Mismatches: 29
 Query Match: 79.15% Indels: 1
 DB: 4 Gaps: 1

US-10-660-499a-2 (1-255) x AAD03712 (1-1103)

QY 4 IleMetLeuValLeuGlySerLeuIleGlyLeuGlyCysPheThrIleThrThrTyrala 23
 DB 51 GTCAATTAGCAATTCGGAATTTATTAATGTTGTGTGCAATTTTCTCCAGTCAATGAT 110

Pt	Gene controlling root development of plant and method for manipulating
Pt	root development of plant using the same to improve phenotype of plant
Pt	related to root development and facilitate its growth.
XX	
PS	Claim 5; SEQ ID NO 1; 27bp; Korean.
XX	
CC	The present invention relates to soybean gene GmEXPL coding sequence
CC	(ADY03860), which encodes the protein expansin (ADY03861), which in turn
CC	controls plant root development. The invention also relates to a method
CC	for manipulating plant root development using GmEXPL expansin, to improve
CC	the phenotype of a plant related to root development, and facilitating
CC	the growth of it. Also disclosed are: recombinant vector pGA643/GmEXPL,
CC	which contains gene GmEXPL; and a transformed bacterium produced by
CC	transforming a bacterium with the recombinant vector pGA643/GmEXPL. The
CC	method for facilitating the root development of a plant comprises
CC	inserting the gene GmEXPL into the expression vector, and introducing the
CC	expression vector into the plant.
SQ	Sequence 1089 BP; 323 A; 225 C; 226 G; 315 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	8, 9e-135 Length: 1089
Score:	1403.00 Matches: 255
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	14 Gaps: 0
US-10-660-459A-2 (1-255) x ADY03860 (1-1089)	
Oy	1 MetGlyLysIleMetLeuValIleuGlySerLeuIleGlyLeuGlyCysPheThrIleThr 20
Dd	52 ATGGCGCAAAATCATAGCTGTGTTTGGGTAGCTCATTGAGATTATGCGTTTCACAAATCACT 111
Oy	21 ThrTYrAlaPheSerProSerGlyTYrPTnAsnAlaHisAlaThrPheTYrGlyIySer 40
Dd	112 ACCTATGCCTTCTCACCTCTGGATGAGCAAGGCCATGCCACTTTTATGGGGTAGT 171
Oy	41 AspaIasergLYThrMetGlyLyalaCyseGLYTyrGlyAsnLeuTYrAlaThrGlyTy 60
Dd	172 GATGCTTCAGAGAACTATGGGGGAGAGCTGTGGGTATGGGAATCTGTATGCACTGGGGTAT 231
Oy	61 GlyTPArGxThralalaleuSerrThralaleuPheAsnAspGlylaseCyseGlyIn 80
Dd	232 GGAACTAGAACGACGACCTTTAGCACTGGCTTTATTAATGATGAGAGCTTCTGAGTCA 291
Oy	81 CyseTYrLysIleIleCYsaSPTYrLYsSerASPSeArGrTPCySileUsgLYArGser 100
Dd	292 TGCTNCAAATTAATTAATGATTAACAATGACATCTAGATNGTGATCAAGAAGATCT 351
Oy	101 ValTHrValTHraIaThraAnPheCySPROTrOAsnPheAlaleuPRObaAsnAngLY 120
Dd	352 GTAAACCGTAACGCCCAAACTTTTGCCCCCTCCCAATTTGCCCTTCTTAACAACAATGGA 411
Oy	121 GlyTRPCyAsnProProLeuLysHIsphEaspMeTAlginPRoIAaITRgJULyVIlle 140
Dd	412 GGCTGGTGAACCCACACACTCAAGCAATTTGATATGAGCCCAACCCTGGGAAAAGATT 471
Oy	141 GlyIleTYrArgGlyGlyIleValProValIleuPheGlnaryValProCYsLYsLYHis 160
Dd	472 GGNATTTACAGAGAGAGATCGTCCCCTGCTATTCCAAGGGTTCATGCAAAAAAGCAT 531
Oy	161 GlyGlyValArgPheSerValangLYAdgaSTYrPhesIleuValIleuIleSerAn 180
Dd	532 GGAAGGGGTAGTTCAGTGTGAATGGAGAGGACATACTTGAAGTATGATCAAGCAAT 591

OY 181 ValGlyGlyAlaGlySerIleGlnSerValPheIleValGlySerIleThrGlyTPmet 200
 Db 592 GTGGGGGGTCTGTGATCCATCCATCACTGATTCATTAAAGCTCAAAAATGATGATG 651
 OY 201 AlawetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaIleTyrIleuansnglyGlnSer 220
 Db 652 GCATGTGCAAGAAATTTGGGGTTCATTATGGCAATCAATGCGTATTTGAATGGTCAATCT 711
 OY 221 LeuserPheArgValThrThrThrAspGlyGluThrArgValPheGlnAspIleValPro 240
 Db 712 TTGTTCCTTCAGGGTCCACACCACTGATGAGAGACAGAGTTCCTCCAAATATATTGTTCCA 771
 OY 241 ValSerTrpThrPheGlyGlyIleThrPheSerSerProValGlnPhe 255
 Db 772 GTAAGTTGACATTCGGCCAAACCTTCTCTAGCCCACTTCAGTTCC 816
 RESULT 2
 ID ADX27747 standard; cDNA; 1134 BP.
 AC ADX27747;
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 10567.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS unidentified.
 XX
 PN US2004034888-A1.
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678. *← KBN C10-68*
 XX
 PA ITUUY/ LIU J.
 PA (ZHOU)/ ZHOU Y.
 PA (KOVA)/ KOVALIC D K.
 PA (SCRE)/ SCREEN S E.
 PA (TABAA)/ TABASKA J E.
 PA (CAOY)/ CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 10567; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring

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OM protein - nucleic search, using frame_plus_p2n model

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Run on:      January 11, 2006, 18:42:35 ; Search time 501 Seconds
              (without alignments)
              3392.209 Million cell updates/sec
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Title: US-10-660-499A-2
Perfect score: 1403
Sequence: 1 MGKIMLVGSLIGHCFTIT.....QDIVPVSMTFGQTSSPVQF 255

Scoring table:		
BLOSUM62		
Xgapop 10.0	Xgapext 0.5	
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

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Searched:      4996997 begs, 3332346308 residues
Total number of hits satisfying chosen parameters:  993994
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/gen2.1/USPFO.pafat.p/US1066496/runat_10012006_105620_16414/app_query.fasta_1.1391
-DB=N Generated -OFMT=fasta -SUPFLX=p2n.rng -MINMATCH=0.1 -LOOCC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi -LIST=45
-DOCKALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1066496@CGEN_1.1.1096@runat_10012006_105620_16414 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESCORE -NEG SCORES=0 -WAIT -DSPLOKLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEAD=6 -DELEXT=7

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Database :
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005a:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1403	100.0	1089	14	ADY03860	Ady03860 Soybean
2	1399	99.2	1134	13	ADx27747	Adx27747 Plant fu
3	1110.5	79.7	1103	4	AA003712	AA003712 Tomato se
4	1098.5	78.3	980	3	AAc11263	AAc11263 Arabidops

5	1091	77.8	759	12	ADN74396	Adn74396	Thale cress
6	1055	75.2	1132	12	ACN38981	Acn38981	Arabidopsis
7	1043	74.3	1010	13	ADX51829	Adx51829	Plant full
8	1043	74.3	1029	13	ADX4182	Adx4182	Plant full
9	1042	74.3	1053	13	ADX54060	Adx54060	Plant full
10	971.5	69.2	789	8	ADA65924	Ada65924	Rice gene
11	960.5	68.5	695	3	ACAC41531	Acac41531	Arabidopsis
12	944	67.3	576	13	ACN646900	Acn646900	Cotton protein
13	944	67.3	601	13	ACN46993	Acn46993	Cotton protein
14	936.5	66.7	753	8	ADA659467	Ada659467	Rice gene
15	913	65.1	1455	13	ADX13859	Adx13859	Plant full
16	906	64.6	904	12	ADJ3951	Adj3951	Plant full
17	900.5	64.2	2139	10	ADOC08361	Adoc08361	Rice DNA
18	898	64.0	780	3	AACS0628	Aacs0628	Arabidopsis
19	898	64.0	1198	3	AAc33521	Aac33521	Arabidopsis
20	898	64.0	1233	3	AAC50633	Aac50633	Arabidopsis
21	898	64.0	1276	13	ADT15760	Adt15760	Plant cDN
22	892.5	63.6	956	6	ADX27589	Adx27589	Plant full
23	890.5	63.5	753	13	ABZ12286	Abz12286	Arabidopsis
24	889	63.4	681	2	AAAT13320	Aaat13320	Cucumber
25	889	63.4	681	6	ABA97162	Abag97162	C. sativu
26	889	63.4	684	6	ABA97161	Abag97161	C. sativu
27	887.5	63.3	756	6	ADAV0190	Adav0190	Rice gene
28	885	63.1	1302	13	ADX14145	Adx14145	Plant full
29	883	62.9	1236	3	AAc40035	Aac40035	Arabidopsis
30	882.5	62.9	783	14	ADZ00474	Adz00474	Expansin
31	882	62.9	1326	3	AAC40169	Aac40169	Arabidopsis
32	881	62.8	1324	3	AAC47530	Aac47530	Arabidopsis
33	879	62.7	735	11	ACT33871	Act33871	Rice abio
34	879	62.5	735	12	AD145678	Ad145678	Corn isop
35	876.5	62.5	747	6	ABZ13264	Abz13264	Arabidopsis
36	876.5	62.5	1167	6	ADAD03713	Adad03713	Tomato se
37	874	62.3	768	6	ABZ13241	Abz13241	Arabidopsis
38	869.5	62.0	792	11	ACT26658	Act26658	Rice abio
39	864.5	61.6	768	11	ACT26574	Act26574	Rice abio
40	864.5	61.6	1366	3	AAc47991	Acac47991	Arabidopsis
41	862	61.4	762	6	ABZ13283	Abz13283	Arabidopsis
42	862	61.4	762	8	ADA68308	Ada68308	Arabidopsis
43	862	61.4	1015	3	AAc48712	Acac48712	Arabidopsis
44	862	61.4	1016	3	AAc40777	Acac40777	Arabidopsis
45	861.5	61.4	1212	3	AAC45165	Aac45165	Arabidopsis

ALIGNMENTS

RESULT 1
ADY03860
ID ADY03860 standard; cDNA; 1089 BP.

AC ADY03860;

DT 21-APR-2005 (first entry)

Soybean expansin, GmEXPI, coding sequence, SEQ ID 1.

KW GmEXP1; expansin; plant; root; development; gene; 88.

OS Glycine max.

FH	Key	Location/Qualifiers
70	010	

```
/*tag= a
```

XX
XX

PD 06-OCT-2004.

PF 27-MAR-2003; 2003KR-00019069.

PR 27-MAR-2003; 2003KR-00019069

PA (UYSE-) UNIV SEOUL NAT IND FOUND.

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Db      531  CCGCGGCGGCGATTGTTCCCGTCAACTCAAAAGGGGCCATGTGTGAAGCAAGGAGGGGT 590
QY      540  TAGGTTTCAGTGTGAATGGAGGAGCACTACTTTGAGCTAGTATGATCAGCAATGTGGGAGG 599
Db      591  GAGGTTTCAACATCAACGGCGGCGGCACTACTTCGAGCTGTGTCTCATCTCCAACGTCCGCGG 650
QY      600  TGCTGCAATCCATCCATCAATCAGTGTTCATTAAAGGCTCAAAAACGTGAATGGCAATGTC 659
Db      651  CTGCGGCTTCATCCAGTCAGTCGCGCGTCGATCAAAAGGATCGAGGACCGGGGTGATGGCCATGTC 710
QY      660  AAGAAATTTGGGGGTTTCAATTGGCAATCCAAATGGGTAATTTGAATGGTCA 707
Db      711  GAGGAACCTGGGGAGTCACCTGGCGCATGTAAACGGTACTTCGACGGGCA 758

RESULT 13
US-10-437-963-33939
; Sequence 33939, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33939
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38002C.1
US-10-437-963-33939

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Query Match	27.1%	Score 295.6	DB 7	Length 1046
Best Local Similarity	65.8%	Pred. No. 5	2e-59	
Matches 446	Conservative 0	Miss Matches 229	Indels 3	Gaps 1
Qy	141	CAAGCCCATGSCAACTTTTATATGAGGGGTAGTGCATCTTCAGGAACTATAGGGGGAGCTTG	200	
Db	135	CAGTGGCAAGGCCACGGCTTCTACGGCGGAGCGAACCCCTTCGGGACAAATGGCGGGCGGTG	194	
Qy	201	TGGGTATGGGAATCTGTATGTGCACTGGGTATGGAACTGAACCTGCAGCTTTAAGCATGCG	260	
Db	195	CGGGTACGGCAACTGTACTGACGGGGGTATCGGAGCGAACAACGGGGCGGTGAGTCCGGC	254	
Qy	261	CTTATTTAATGATGAGAGCTTCCTGTGTGTCAGTGTCTACAAATTAATATGTGATTACAAATC	320	
Db	255	GCTGTTCAACGACGGCGCGCGGTGGCGGAGTGTCAACAGATCAACGTGCG---ACCAAGTC	311	
Qy	321	AGACTTATGATGTGTGCATCAAAAGGAAGATCTGTAACTGTAACTGCACAAACTTTTGCC	380	
Db	312	CAACTCGAAGTGTGTCAAGGGCGGCGACGTGGTGCATCAACCGGAGCAACACTCTGCCC	371	
Qy	381	TCCCAATTTGGCCCTTCTTAACAACAATGAGAGGCTGGTGCAACCAACACTCAAGCATTT	440	
Db	372	ACCGGACTACTTCCAAAGCCGAGACGACGAGCGGGCTGTGTGCACCCGCCGCGCAGACATT	431	
Qy	441	TGATATGGCCCAACCCGCTTGGGAAAGATTGTATTTCAGAGGAGGGATGTCCCGT	500	
Db	432	CGACATGGCGCAACCCGCTGGGAACAATGGCGCTTCAACGGCGGCGCATGTCCCGT	491	
Qy	501	GCTATTTTCAAAAGGTTCCATGCAAAAAGCATGAGAGGGTTAGTTCACTGATGCAATGGGAG	560	

Accession	Sequence	Position
Db	CAATTTCCAGAGGGTGTGTGACAGAGGAAAGAGGGGTGAGTTTCACATCAACGGGAA	551
Qy	561 GGAATCTTTGAGGATGATTTGATACAGCAATGTGGGGGGTGTCTGGATCCATCCAAATGAT	620
Db	552 CAGCTACTTCAGAGCTGGTGTCTGATACCAAGTGGGCGGGCGGGGTTCGATCAAGTGGT	611
Qy	621 GTTCATTAAAGGCTCAAAACTGATGTGATGGCAATGTCAGAAATTGGGGTTCATAATG	680
Db	612 GCAGATCAAGGGAAACAAAGACGGGGTGGGTGACATGTCGGGAACTGGGGCGCCAACTG	671
Qy	681 GCATTCGATGGCTATTGAAATGTCATCTTTGTCTTCAAGGGTCCACCACTGATGG	740
Db	672 GCAGCGCAACACTACTCTACACACACAGGCCATCTCTTCTCGGTCACTTCCACCGCCGG	731
Qy	741 AGAGACCAAGTTCCTCCAGATATTTGTTCCAGTAAAGTTGACATTTTGGCCAACTTTCTC	800
Db	732 CAAGACGCTGTCTTCAGAGACGTGGCCCGTCCAACTGGCAATTCGGCCAGACATTCAC	791
Qy	801 TAGCCCAATTCAGTTCTTA	818
Db	792 CAGCGCGGTGCAGTTCTTA	809

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RESULT 14
US-10-437-963-29573
; Sequence 29573, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29573
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34061C.1
US-10-437-963-29573

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Query Match	27.0%	Score 294.2	DB 7	Length 1204
Best Local Similarity	65.1%	Pred. No. 2.1e-58		
Matches	450	Conservative 0	Mismatches 238	Indels 3
			Gaps	1
QY	133	GGATGAGCAACGGCCATGACCTTTTATATGGGGGTAGTGATGCTTCAGAACTATGGGG	192	
Db	203	GGGTGGGTGAAGGGGCGCACGCCACGTTCTTACGGCGGGCGGACCGGTCCGGGAACATGGGC	262	
QY	193	GGACCTTGTGGGTATGGGATCTGTATGCACTGSGTATGGAATGAACTGCAGCTTTA	252	
Db	263	GGGGCGTGGGGTACGGCACTGTACCGCGAGGGGTACGGCAGAGGAGCGGGCGGCTC	322	
QY	253	AGCATGCGCTTATTTATGATGAGAGCTTCTGTGGTCAAGTCTCAAAATTAATATGTGAT	312	
Db	323	AGCACGGCGCTTTCAACGAGCGGCGTGGCTGGCGGGCAGTCTCAAGAGCTGTGCGAC	382	
QY	313	TACAAATCAGACTTAAGTGGTGGCATCAAGAAGATGTGTAACGTAACTGCCACAAC	372	
Db	383	CGAAGAGGAGCCGGACGTGGTGAAGCGGGCGTCTTCGTACACATACCGCCACCAAC	442	
QY	373	TTTGGCCCTCCCAATTTGACCTTCTCTTAACAACATGAGGCTGGTGCAACCCACACTC	432	
Db	443	TTTGGCCCGCCCAACTGGAGCTTCCCGACGACACAGCGGGCTGGTGCACCCGCGCGC	502	

Db 104 CTTTCTTAAGTGAATGTTTTCAGAGATTCTGGATGTCAGATGCTCATGCCACA 163
Qy 157 TTTTATGGGGGTAGTATGCTTTCAGAACTATGGGGGAGCTGTGGTATGGGAATCTG 216
Db 164 TTTTATGGGTGAGCTGATGCTTCTGCGACCATGGGGGTGCTTGTGATATGGAACCTG 223
Qy 217 TATGCAACCTGGTATGGAACCTGCACTGGCTTTAGCACTGGCTTATTAATGAGGA 276
Db 224 TATTCACAGGGATGGAACAAGGACAGCTGATGCACTGATGTTCAATGATGGA 283
Qy 277 GCTTCTGTGATGATGCTCAAAATATATGATATACAAATGAGACTGATAGTGTGC 336
Db 284 GGAATCCTGTGGCCATGCTCAAGATCATATGATATATAAGGAGACCCCGATGCTGC 343
Qy 337 ATCAAGAGAGATCTGTACCCGTACTGCCAACAATCTTTCCTCCCAATTTGGCCCTT 366
Db 344 AAAAAAGGAGTATCTGTACATTAACATCAAAATTTTGGCCACCAAAATTAACATCTT 403
Qy 397 CCTAACAAAGAGAGGCTGTGCAACCACTCAAGCATTTTATGATGGCCCAACC 456
Db 404 CTTAGTACAAATGAGGCTGTGTACCCCTCTGCTCCCAATTTGACATGGCTCAACCT 463
Qy 457 GCTTGGAAAAAGATGTTATTTTACAGAGAGGATCGTCCCGCTATTTTCAAGGGTT 516
Db 464 GCTTGGAAAAAGATGTTATTTTACAAAGAGGATTTCTGTGCTCTACAAAGGGTT 523
Qy 517 CCATGCAAAAAAGATGAGGGGTTAGGTTCACTGTGTAATGGAGGACTATCTTGAGCTTA 576
Db 524 CTTGGCAAGAAAGAACTGAGATGATGATCAACATCAATGGAAGGACTATTTTGAACCTA 583
Qy 577 GTATTTATCAAGCATGTGGGGGCTGTGATCCATCCAAATCACT 620
Db 584 GTCTTGTAGCAATGATGACAGGGGAGATCTGTCAATCTGT 627

RESULT 11

US-10-424-599-49748
; Sequence 49748, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Roca Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 49748
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_15931C.1
US-10-424-599-49748

Query Match 29.5%; Score 321.4; DB 7; Length 518;
Best Local Similarity 82.8%; Pred. No. 6e-65;
Matches 380; Conservative 0; Mismatches 76; Indels 3; Gaps 1;
Qy 41 AAAAAAATATGGGCAAAATCATGCTGTTTGG---GTAGCTCATTTGATTAATGCT 97
Db 60 AAAAGATCTAATGCGCTAAAGTCAATGTTGGTTGGCTGCTCAAGCTTCTCTGATTAATGCT 119
Qy 98 GTTTCACATCACTACTATGCTTCTCACTTCTGATGAGCAACGCGCATGCACTT 157
Db 120 GTTTCACATCACTACTAGCGCTTCTCACTTCTGATGAGCAACGCGCATGCACTT 179
Qy 158 TTTATGGGGGTAGTATGCTTTCAGAGAACTATGGGGGAGCTTGTGGTATGGGAATCTGT 217
Db 180 TTTATGAGGTAGCTAGTCTCGGGGACATGGGAGAGACTTGTGGGTATGGGAATCTGT 239

Qy 218 ATGCACTGGGTATGGAACCTAGACTGACCTTTAAGCACTGCTTATTTAATGATGAG 277
Db 240 ATTGCAAGGGTACGGAACGATATACAGCGGCTTAATGATCTGCATATTTAAGATGAG 299
Qy 278 CTTCTGTGCTGATGCTCAAAATATATATGATATACAAATATAGACTAGATGGTGA 337
Db 300 CTTATGTTGGGAGTGTTCATTAATCATATGCAATTTATCAAAAGATCCAGATGGTGT 359
Qy 338 TCAAGAGAGATCTGTACCGTAACTGCACAAACTTTTGGCCCTCCCAATTTGGCCCTTC 397
Db 360 TGAAGGAGCATCATATACATTAATGCAACAACTTCTGCTCCCAATTTTGGCTTTC 419
Qy 398 CTACACCAATGAGAGCTGTGTGACACCCACATCTCAAGACTTTGATATGGCCCAACCG 457
Db 420 CCAACACACAGAGAGATGTGTGCAACCCACTCTCAAACTTTGACATGTGCTCAACCCG 479
Qy 458 CTTGGAAAAAGATGTTATTTTACAGAGAGGAGATGCTCC 496
Db 480 CATGGAAAAAGATTTGATTTATCTATCGAGAGGAGATCTGTC 518

RESULT 12

US-10-767-701-14995
; Sequence 14995, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14995
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1058_2
US-10-767-701-14995

Query Match 28.3%; Score 308; DB 7; Length 765;
Best Local Similarity 70.2%; Pred. No. 9.9e-62;
Matches 413; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
Qy 120 CTTCTACCTTCTGATGGAACAAGCCCAATGCACTTTTATGGGGGTATGATGCTTC 179
Db 171 CTTCTGCGGTCCGCGCATGAACAAGCGTTCGCACTTTCTACGCGGTAGCGACGCTTC 230
Qy 180 AGGAATATATGGGGGAGCTTGGGTTATGGGAATCTGTATGCACTCGGGATATGGAATGAG 239
Db 231 AGGAAGATGAGGTGGAGCTTGTGGTATGGAACCTGTACTGACGCGGTACCGACGAA 290
Qy 240 AACTGAGCTTTAAGCACTGCTTATTTATGATGAGAGCTTCTGTGTCAAGTGTACAA 299
Db 291 CAGCGGCGCTGAGACAGCGCGCTGTTCACAGACGCGCTGTGCGGAGAGTCTACCG 350
Qy 300 AATTATATGTATTAACAACTCAAGACTCTAGATGATGATCAAGAGAAATCTGTAACTGT 359
Db 351 GATCTGTGCACTACCAAGCGGAGCCGCGGTCTGTCATCTCGGCGACGTCGGTGAACAT 410
Qy 360 AACTGCACAAACTTTTGGCTTCCCAATTTGCGCTTCTTAACAACAATGAGAGCTGTG 419
Db 411 CAGGCAACAACCTTTTGGCTTCCCAACTACAGCGCTGCCAAGCAGAGCGCGCTGTG 470
Qy 420 CAACCAACAACCAAGCACTTTTATGATATGAGCCCAACCGCTGTGGAAAAAGATTTGATTTA 479
Db 471 CAACCGCGCGCGAGCACTTGTGACATGGCCAGCGCGCTTGTCTCAAGATGGCAATCTA 530
Qy 480 CAGAGAGGATGATGCTCCGCTATTTTCAAGAGGTTTCATGCAAAAAAGATGAGAGGAT 539


```
QY 540 TAGGTCAGTGTGAAATGAGGAGGAGCTATTGAGCTAGTATTGATGAGCAATGAGGAGG 599
    |||||
Db 583 GAGGTTGAGATCAAGGAGGAGGAGCTACTGAGCTGAGTGTCTCATCTCAACGTTGAGCG 642
QY 600 TGCTGATCCATCAATCAAGTGTTCATTAAAGGCTCAAAAATCGATGAGTGAATGTC 659
    |||||
Db 643 CTGCGGATCATCACTGAGCTGAGCTGATCAAGGGGTGCGGACCGGGTGAATGGCATGTC 702
QY 660 AAGAAATGGGGGTTCTTAATTTGGCAATCCATGCGTATTTGAATGTCATCTTTGCTCT 719
    |||||
Db 703 CCGAATCTGGGGGCTCAACTGCGAGTCCAAAGCGTACTCAATGAGCCAGAGCTGCTGCT 762
QY 720 CAGGTCACCAACCACTGATGAGAGACCAAGTTTCCAAAGATTTGTTCCATTAATGTTG 779
    |||||
Db 763 CCAAGTCACCAACCAAGAGCGGCGCAACCAAACTTCCCGAGCTGCGCCCGCAGCTG 822
QY 780 GACATTCGGCCAAATTTCTCTAGCCAGTTCAGTTCT 817
    |||||
Db 823 GGGGTTCTGGTCAGACGTTTGGACCTGCGACAGCTCT 860
```

RESULT 9

```
US-10-437-963-100529
; Sequence 100529, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 100529
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98236C.1
US-10-437-963-100529
```

```
Query Match 30.6%; Score 333; DB 7; Length 1187;
Best Local Similarity 66.2%; Pred. No. 1.7e-67;
Matches 480; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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QY 93 ATGCTGTTTCAATCAATCACTATGCTTCTCACTTCTGATGAGCAACGCCCATGTC 152
    |||||
Db 83 ATGCTCTCTTGAGAACGAGGCCGATGTTCAAGGCTCGGGCTGAAACAAGGGTTGCG 142
QY 153 CACTTTTATGGGGGATGATGCTTCAAGAACTATGAGGAGAGCTTTGAGGATGAGAA 212
    |||||
Db 143 CACTTCTACGGCGGAGTACGCTTCAAGAACGATGGGCTGAGGCTGTTGAGTACGGGGA 202
QY 213 TCTGTATGCAATCGGATGAGAACTAGAACTGACGCTTTAAGCACTGCTTATTATTA 272
    |||||
Db 203 CTGTATCTGACGGGATGAGGAGCAACGAGCGGCTGAGCAAGGTTGCTGTCAACGA 262
QY 273 TGAAGCTTCTGAGTGTGATGCTTCAAAATATATGATTAATCAAGCTCTAGATG 332
    |||||
Db 263 CCGGGCTCTGAGCGGAGAGTCTTACCGGATCATGTGGACTACAGGCGGAGCGGCTT 322
QY 333 GTGATCAAAAGAAAGATCTGTACCGTACTGCAAACTTTTGCCCTCCCAATTTGCG 392
    |||||
Db 323 CTGATCTCGGAGCGTCTGAGTACATCAAGGCAACAACTTGTCCCGCAACTACGCG 382
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QY 393 CCTTCTTAACAAATGAGAGGCTGTGCAACCCACATCAAGCAATTTTGAATGAGCCA 452
    |||||
Db 383 GCTCCCAACGAGCGCGGGGTGTGCAACCCGCGGAGCACTTGCACATGAGCCGA 442
QY 453 ACCCGTTGGGAAAAGATTGTATTTATCAAGAGAGGAGATCTGTCCTGCTATTTAAAG 512
    |||||
Db 443 ACCGCGTGTGCTCAAGATCGGCTCTACGTGCGCGGATCTGTCCGATGTATCAAGCG 502
QY 513 GGTTCATGCAAAAAGCATGAGAGGGTGTAGTTAGTGAATGGAATGAGAGGAACTACTTGA 572
    |||||
Db 503 GGTGCGGTGCGCAACAGAGGAGGAGTGAAGTTCAACATCAACGAGGAACTACTTGA 562
QY 573 GCTAGTATGATCAGCAATGTGAGGAGTGTGATGATCATCAATCAATGATTTAAAG 632
    |||||
Db 563 GCTGAGTCTGCTCTCAAGCTGCGGCGCTGCGCTCACTCAAGTGTGTCAATCAAGG 622
QY 633 CTCAAAACTGATGAGATGAGCAATGTCAAGAAATTTGGGTTTAAATTTGCAATCAATG 692
    |||||
Db 623 GTGAGAGACCGGGTGTGATGAGCATGTCCAGAAATTTGGGCTGTCAATGAGCAAGCG 682
QY 693 GTATTTGAATGTCATCTTTGCTTCAAGGTCACACCACTGATGAGAGACCAAGAT 752
    |||||
Db 683 CTACCTGACCGGCAAGGCTGTCTTCAAGGTCAACAGACGAGAGCGGCAAGCTCAC 742
QY 753 TTTCCAAAGATATTGTTCCAGTAAAGTTGACATTCGAGCAATTTCTAGCCAGTTCA 812
    |||||
Db 743 CTTCCTGACGTCGCGCGGCGGCTGAGAGTTCGAGCTTCTGACCTCAAGCA 802
QY 813 GTTCT 817
    |||||
Db 803 GTTCT 807
```

RESULT 10

```
US-10-487-901-7077
; Sequence 7077, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: McCreary, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Meglarz, Thadeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7077
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7077
```

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Query Match 29.7%; Score 323.2; DB 9; Length 634;
Best Local Similarity 73.3%; Pred. No. 2.5e-65;
Matches 428; Conservative 0; Mismatches 153; Indels 3; Gaps 1;
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```
QY 40 CAGAAAAAATGAGCAAAATCAATGCTGTTTGGGATGAGCTCATGATGATGATGCTGT 99
    |||||
Db 44 CTAAAGAAAATGCTAAATCAATGCAATTTGCACTGGAGATTCATTAATTTGTTGTGCAAC 103
    |||||
QY 100 TTCAATCACTACATGATGCTTCTCAC--TTCTGAATGAGCAACGCCCATGCACT 156
    |||||
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Db      690 CCGGAAGTGGGGGTCACTGGGATGCAAGCGTACTTAATGCGCAAGCCGTGCTT 749
Qy      720 CAGGGTCACCAACCATGATGAGAGACAGAGTTTTCAGAGATATGTTCCAGTAAGTTG 779
Db      750 CCAAGTCACCAAGAGAGAGCGGCGCAAGCAAAACCTTCCCGAGCGTCCGCCAGAGCTG 809
Qy      780 GACATTCGGCCAAACTTCTCTAGCCCAAGTTCAAGTTCT 817
Db      810 GGGGTTCCGTCAGACGTTTGGCAGCTCGACAGAGTTCT 847
```

RESULT 7

```
US-10-425-114-17012
; Sequence 17012, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 17012
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
```

```
; OTHER INFORMATION: Clone ID: LIB3067-046-E8_FLI
US-10-425-114-17012
```

```
Query Match      30.7%; Score 334.8; DB 7; Length 1029;
Best Local Similarity 67.5%; Pred. No. 5,9e-68;
Matches 471; Conservative 0; Mismatches 227; Indels 0; Gaps 0;
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```
Qy      120 CTCTCACTCTTGATGAGCAACGCCCATCTTTTATGAGGGGTAGTATGCTTC 179
Db      146 CTCTCGGGGTCCGGCTAAACAAGGCTTCGACCTTCTATGCGGTAGCGACGCTTC 205
Qy      180 AGGAATATGAGGGGAGCTGTGAGTATGGAATCTGTATGCAACTGCGGTAGGAATAG 239
Db      206 AGGAATGATGAGGGGAGCTGTGAGTATGGAATCTGTATGCAACTGCGGTAGGAATAG 265
Qy      240 AACTGAGCTTTAAGCACTGCTTATTTAATGATGAGCTTCTGTGTCAGTGTACAA 299
Db      266 CACGGGGGCGGTAGAGCAGCGGCTCTTCAACGACGCGGCTCGTGGGGGAGTACACG 325
Qy      300 AATTATATGATTAACAATCAGACTCTAGATGATGATTAAGAAAGAAATCTGTAAACGT 359
Db      326 GATCTCTGTGACTACAGGCGGACCGGCTTCTGATCCGCGGACGTCGTGACAT 385
Qy      360 AACTGCACAAACTTTTGGCTCCCAATTTGCGCTTCTTAACAACAATGAGGCGTGGT 419
Db      386 CACCGCAACCAACTGTGCTCTCCCAACTACGCGCTGCGCAACGACGCGCGCTGGT 445
Qy      420 CAACCCACCACTCAACATTTTATGATGAGCCCAACCGCTTGGGAAAAGATTGTAATTA 479
Db      446 CAACCGCGCGGCGGACAGCACTTGACATGCGGAGCGCGCTGGCTCAAGATGCGCATCTA 505
Qy      480 CAGAGAGAGGATGTCCTCCGCTGCTATTTCAAGAGGTTCCATGCAAAAAGATGAGAGGT 539
Db      506 CCGCGCGCGGATGTCCTCCGCTGCTAATCAACAAAGGTCCTGTGTGAAAGAAAGCGGAGT 565
Qy      540 TGGGTCAGTGTGATGAGGAGGAGCTACTTTGAGCTAGTATGATCAGCAATGTTGGGGGT 599
Db      566 GAGGTTCAAGATCAACGGGGCGGACATCTTCAAGCTGAGTCTATCTCAACGTTGGGCGG 625
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Qy      600 TGCTGATCCATTCATCAAGTGTCTATTAAGGCTCAAAAACCTGATGATGAGCAATGTC 659
Db      626 CTGCGGGTCATCTCACTGCGCGCTCATCAAGGGGTGCGCACCGGGTGAATGSCCATGTC 685
Qy      660 AAGAAATGAGGGGTTTAAATTTGCAATTCAGTGGATTTGAATGATCAATCTTTGCTCT 719
Db      686 CCGGAAGTGGGGGTCAACTGGGATGTCACAGCGTACCTCAATGCGCAGAGCCTGTGCTT 745
Qy      720 CAGGGTCACCAACCATGATGAGAGACAGAGTTTTCAGAGATATGTTCCAGTAAGTTG 779
Db      746 CCAAGTCACCAAGAGAGAGCGGCGCAAGCAAAACCTTCCCGAGCGTCCGCCAGAGCTG 805
Qy      780 GACATTCGGCCAAACTTCTCTAGCCCAAGTTCAAGTTCT 817
Db      806 GGGGTTCCGTCAGACGTTTGGCAGCTCGACAGAGTTCT 843
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RESULT 8

```
US-10-425-114-28800
; Sequence 28800, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 28800
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
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; OTHER INFORMATION: Clone ID: LIB4764-020-G11_FLI
US-10-425-114-28800
```

```
Query Match      30.7%; Score 334.8; DB 7; Length 1053;
Best Local Similarity 67.5%; Pred. No. 6e-68;
Matches 471; Conservative 0; Mismatches 227; Indels 0; Gaps 0;
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```
Qy      120 CTCTCACTCTTGATGAGCAACGCCCATCTTTTATGAGGGGTAGTATGCTTC 179
Db      163 CTCTCGGGGTCCGGCTAAACAAGGCTTCGACCTTCTATGCGGTAGCGACGCTTC 222
Qy      180 AGGAATATGAGGGGAGCTGTGAGTATGGAATCTGTATGCAACTGCGGTAGGAATAG 239
Db      223 AGGAATGATGAGGGGAGCTGTGAGTATGGAATCTGTATGCAACTGCGGTAGGAATAG 282
Qy      240 AACTGAGCTTTAAGCACTGCTTATTTAATGATGAGCTTCTGTGTCAGTGTACAA 299
Db      283 CACGGGGGCGGTAGAGCAGCGGCTCTTCAACGACGCGCTCGTGGGGGAGTACACG 342
Qy      300 AATTATATGATTAACAATCAGACTCTAGATGATGATTAAGAAAGAAATCTGTAAACGT 359
Db      343 GATCCCTCGACTACAGGCGGACCGGCTTCTGATCCGCGGACGTCGTGACAT 402
Qy      360 AACTGCACAAACTTTTGGCTCCCAATTTGCGCTTCTTAACAACAATGAGGCGTGGT 419
Db      403 CACCGCAACCAACTGTGCTCTCCCAACTACGCGCTGCGCAACGACGCGCGCTGGT 462
Qy      420 CAACCCACCACTCAACATTTTATGATGAGCCCAACCGCTTGGGAAAAGATTGTAATTA 479
Db      463 CAACCGCGCGGCGGACAGCACTTGACATGCGCGGCTGGCTCAAGATGCGCATCTA 522
Qy      480 CAGAGAGAGGATGTCCTCCGCTGCTATTTCAAGAGGTTCCATGCAAAAAGATGAGAGGT 539
Db      523 CCGCGCGCGGATGTCCTCCGCTGCTAATCAACAAAGGTCCTGTGTGAAAGAAAGCGGAGT 582
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Db 541 GTTTGGCCAGACTTCTCTAGCAAACTACATTTCT 576

RESULT 5

US-10-425-114-26569
; Sequence 26569, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26569
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4315-040-B12_FLI
US-10-425-114-26569

Query Match 30.9%; Score 336.4; DB 7; Length 1010;
Best Local Similarity 67.6%; Pred. No. 2.5e-68;
Matches 472; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 120 CTCTCAGCTTTCGATGAGCAACGCCCACTTTTATGAGGGGTAGTGGCTTC 179
DB 140 CTCTCGGCGTCCGGCTTAACAGGCGTTCGCCACTTCTATGCGGTAGCCAGCTTC 199
QY 180 AGGAATATGAGGGGAGACTTGTGGTATGGAATCTGTATGCAACTGGGTATGGAATAG 239
DB 200 AGGAACATGAGGTGGGCTGTGGGTACGGCACTGTACTGCAAGGGGTACGGCAGGA 259
QY 240 AACTGACGCTTAAAGCACTGCTTATTTATGATGAGAGCTTCTGTGTCTAGTGTCTCA 299
DB 260 CACGGCGGCGCTGAGCAGCGGCTTTCACAGCGGCGCTGTGGCGGCGAGTGTCTACCG 319
QY 300 AATTATATGATTAACAATCACTAGTGTGATGATCAAGAAAGATCTGTAAACGT 359
DB 320 GATCTCTGAGACTACAGGCGGACCGCGGTCTGTGATCCGCGCAGCTGCGTACAT 379
QY 360 AACTGCCAACAATTTTGCCCTCCCAATTTGCGCCTTCTTAACAACAATGAGGCTGTG 419
DB 380 CACGCCACCACTGTGCTCTCCCACTAGCGCTCCCAACAACAAGCGGCTGTG 439
QY 420 CAACCAACAATCAAGCAATTTGATGATGACCAACCGCTTGGGAAAAAGATGTATTTA 479
DB 440 CAACCGCGCGGAGGACCTTCAATGAGCGGACCGGCGCTGCTCAAGATCGCATCTA 499
QY 480 CAGAGAGGAGTGTCTCCCGTGTATTTCAAGAGGTTCATGCAAAAAGCATGAGGGGT 539
DB 500 CCGGCGGCGGATCTGTGCGCTCAACTACCAAGGGGTGCGGTGTGAAGAAAGCGGGGT 559
QY 540 TAGGTGAGTGTGAATGAGGAGGACTACTTGAAGTGTATTTGATGAGCAATGAGGGGG 599
DB 560 GAGGTTCAGATCAACGGGCGGACACTACTTGAAGTGTGTCTCATCTTCATATGCGCGG 619
QY 600 TGCTGATTCATCAATCAATGATTCATTTAAAGGCTCAAAAATGATGATGAGCATGTCT 659
DB 620 CTGGGGGTCCATTCAGTCCGGGTCTCATCAAGGGGTGCGGACCGGGTGTGATGCGCATGTCT 679
QY 660 AAGAAATTTGGGTTCTAATTTGGCAATCAATGCGGTATTTGAATGTCAATTTTGTCTCT 719
DB 680 CCGGAATGGGGGTCTCAATGCGAGTCCAGCGGTACTCAATGAGCCAGACCTGTGCTT 739

QY 720 CAGGTCACCACTGATGAGAGACCAAGATTTTCCAAAGATTTTCCAGTAACTTG 779
DB 740 CCAGGTCAACCAAGAGGAGCGGCGGACCAAACTTCCCGGACGTGCGCGCGGAGCTG 799
QY 780 GACATTCGGCCAACTTTCTCTAGCCCACTTCACTTCT 817
DB 800 GGGGTTCGTCAGACCTTTGCGACCTTCGAGCAGCTTCT 837

RESULT 6

US-10-425-115-170810
; Sequence 170810, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 170810
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87357C.1
US-10-425-115-170810

Query Match 30.9%; Score 336.4; DB 8; Length 1135;
Best Local Similarity 67.6%; Pred. No. 2.6e-68;
Matches 472; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 120 CTCTCAGCTTTCGATGAGCAACGCCCACTTTTATGAGGGGTAGTGGCTTC 179
DB 150 CTCTCGGCGTCCGGCTTAACAGGCGTTCGCCACTTCTATGCGGTAGCCAGCTTC 209
QY 180 AGGAATATGAGGGGAGACTTGTGGTATGGAATCTGTATGCAACTGGGTATGGAATAG 239
DB 210 AGGAACATGAGGTGGGCTGTGGGTACGGCACTGTACTGCAAGGGGTACGGCAGGA 269
QY 240 AACTGACGCTTAAAGCACTGCTTATTTATGATGAGAGCTTCTGTGTCTAGTGTCTCA 299
DB 270 CACGGCGGCGCTGAGCAGCGGCTTTCACAGCGGCGCTGTGGCGGCGAGTGTCTACCG 329
QY 300 AATTATATGATTAACAATCACTAGTGTGATGATCAAGAAAGATCTGTAAACGT 359
DB 330 GATCTCTGAGACTACAGGCGGACCGCGGTCTGTGATCCGCGCAGCTGCGTACAT 389
QY 360 AACTGCCAACAATTTTGCCCTCCCAATTTGCGCCTTCTTAACAACAATGAGGCTGTG 419
DB 390 CACGCCACCACTGTGCTCTCCCACTAGCGGCTCCCAACAACAAGCGGCTGTG 449
QY 420 CAACCAACAATCAAGCAATTTGATGATGACCAACCGCTTGGGAAAAAGATGTATTTA 479
DB 450 CAACCGCGCGGAGGACCTTCAATGAGCGGACCGGCGCTGCTCAAGATCGCATCTA 509
QY 480 CAGAGAGGAGTGTCTCCCGTGTATTTCAAGAGGTTCATGCAAAAAGCATGAGGGGT 539
DB 510 CCGGCGGCGGATCTGTGCGCTCAACTACCAAGGGGTGCGGTGTGAAGAAAGCGGGGT 569
QY 540 TAGGTGAGTGTGAATGAGGAGGACTACTTGAAGTGTATTTGATGAGCAATGAGGGGG 599
DB 570 GAGGTTCAGATCAACGGGCGGACACTACTTGAAGTGTGTCTCATCTTCATATGCGCGG 629
QY 600 TGCTGATTCATCAATCAATGATTCATTTAAAGGCTCAAAAATGATGATGAGCATGTCT 659
DB 630 CTGGGGGTCCATTCAGTCCGGGTCTCATCAAGGGGTGCGGACCGGGTGTGATGCGCATGTCT 689
QY 660 AAGAAATTTGGGTTCTAATTTGGCAATCAATGCGGTATTTGAATGTCAATTTTGTCTCT 719

QY	908	TATTCCCATCAACTCCAGCCCTCATATCAAGCAATAATTCGTATCATAAT -ACAATCA	966
Db	1017	TATTCCCATCAACTCCAGCCCTCATATCAAGCAATAATTCGTATCATAATACAAATCA	1076
QY	967	ATCAGCATCATATCATCTAAGCTTGATATCAATAAACAATCTTTCAAGTTTAAT	1024
Db	1077	ATCAGCATCATATCATCTAAGCTTGATATCAATAAACAATCTTTCAAGTTTAAT	1134

RESULT 3
US-10-03

```

/ Sequence 1684, Application US/10021323
/ Publication No. US20040123340A1
/ GENERAL INFORMATION:
/ APPLICANT: Deilman, Jill
/ APPLICANT: Feng, Paul C.C.
/ APPLICANT: Pincher, Karen L.
/ APPLICANT: Ziegler, Todd E.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(52274)B
/ CURRENT APPLICATION NUMBER: US/10/021,323
/ CURRENT FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: US 60/255, 619
/ PRIOR FILING DATE: 2000-12-14
/ NUMBER OF SEQ ID NOS: 17880
/ SEQ ID NO 1684
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3825-005-Q1-K6-H7
/ US-10-021-323-1684

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Query Match 34.1%; Score 371.6; DB 7; Length 601;

OY	242	CTGCAAGCTTTAAGCATCTGCTTTATTATTAATGAGAGCTTCGATGAGTCAATCAAA	301
Db	1	CGGCGCGGGGGTACTGCTCTGTTCATTAATGAGAGCTTCATGCGGACAATGCTATTAAGA	60
OY	302	TTATATGATTTACAAATCAGACTCTAGATGGTGCATAAAGAGATCTGTAAACCTTAA	361
Db	61	TCATGTGTGACTATCAGACAGATCCAGATGGTGCATTAAGAGAACATCCGTGACATTA	120
OY	362	CTGCCAACAATCTTTGGCCCTCCCAATTTGCGCCCTTCTTACACAATGAGAGGCTGTGCA	421
Db	121	CAGCAACAACATTTTGTCTCTCTTAATTGTGCTCTCCCAACAACTGCCGAGGCTGTGTCA	180
OY	422	AACCAACCACTGAAGATTTTGTATATGGCCCAACCGCTGGGAAAAGATTGGTATTACA	481
Db	181	ATCCACCCCTCAGACACTTCGACATGGCTCAGCTGCGCGGAAAAAGATTGGTATCTACA	240
OY	482	GAGAGGAGATCGTCCCGCTGCTATTTCAAAGGGTTCATGCAAAAAGCATGAGGGGCTTA	541
Db	241	GAGGGGAATGTGTGCCGTTTGTTCCAAAGGTTCTTGCACAGAGCATGCTGTGAGTGA	300
OY	542	GGTTCAGTGTGAATGGAGAGGACTTCTTGAAGCTAGTATTGATCAGCAATGTGGGGGTG	601
Db	301	GGTTCACATCATGGAAGAGACTTTTCAGCTGTATTATGATTTAGCATGTGGTGGCG	360
OY	602	CTGATTCATCCAAATCAGTGTTCATTAAAGGCTCAAAAATGGAAGATGCGAATGTCAA	661
Db	361	CAGGATCTATCCAGTCTGTGTTCATCAAGGGCTCCAAAATGGGGTGAATGGCAATGTCAA	420
OY	662	GAATATGGGGTCTTATATGGCAATCCAAATGCGTATTTGAATGGTCAATCTTGTGCTTCA	721
Db	421	GGAATGGGGAGACTTACTGTGCAATCATGCTTATCTCAATGGCCAAATCATTTGTGCTTCA	480
OY	722	GGGTCAACCAACTGATGAGAGACCAAGATTTTCCAAATATTGTTCAGTAAAGTTGGA	781

Db 481 GGGTCAACACTCTGATGCTGACTCGTCTAATTTTCTGACATGCTGCGAAATTGGG 540

Qy 782 CATTGGCCAACTTTCTTAGCCAGTTCACTTAAGCTGATTA 827

Db 541 GTTTTGCCAGACTTCTTAGCAAACTACAAATTTAAGATTAGTA 586

RESULT 4
US-10-021-323-1681

```

, Sequence 1681, Application US/10021323
, Publication No. US20040123340A1
, GENERAL INFORMATION:
, APPLICANT: Deikman, Dill
, APPLICANT: Feng, Paul C.C.
, APPLICANT: Fincher, Karen L.
, APPLICANT: Ziesler, Todd E.
, TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
, TITLE OF INVENTION: Plants
, FILE REFERENCE: 38-21(52274)B
, CURRENT APPLICATION NUMBER: US/10/021.323
, CURRENT FILING DATE: 2001-12-12
, PRIOR APPLICATION NUMBER: US 60/255, 619
, PRIOR FILING DATE: 2000-12-14
, NUMBER OF SEQ ID NOS: 17880
, SEQ ID NO 1681
, LENGTH: 576
, TYPE: DNA
, ORGANISM: Gossypium hirsutum
, FEATURE:
, OTHER INFORMATION: Clone ID: LIB3825-005-01-K6-G8
US-10-021-323-1681

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Query Match	33.6%	Score 366.4	DB 7	Length 576
Best Local Similarity	77.3%	Pred. No. 1.8e-75		
Matches 445; Conservative	0	Mismatches 131	Indels 0	Gaps 0

Qy	242	CTGACACTTAAAGCACTGCTCTATTATTANAGAGAGCTCCTGGTGCATGCTCAAGAAA	3010
Db	1	CGGCACCGGGGGTACTGCTCTGTTTCATTAATGAGCTTCAATGGGACAAATGGCTATTAAGA	60
Qy	302	TTATATGTGATTAACAAATACAGACTCTAGATGGTGATCAAGAAGATCTGTAAACGTAA	3610
Db	61	TCATGTGTACATCTCAGACAGATGCCAATGTGTGATTAAGAAGAACTCCGTACCATTTA	120
Qy	362	CTGCCCAAACTTTTGCCCTCCCAATTTCCGCTTCTTAACAACAATAGAGGCTGTGCA	4210
Db	121	CAGCAACAACTTTGTCTCTCTTAACCTTGTGCTTCCCAACAAATGCCGAGGCTGTGCA	180
Qy	422	ACCCACCACTCAAGCACTTTGTATATGAGGCCCAACCCGCTGTGGAAAAATTTGTATTTACA	4810
Db	181	ATCACCCCTCCAGCACTTCGACATGGGCTCAGCCCTGTGGAAAAATTTGTATTTACA	240
Qy	482	GAGAGAGATGTCGCCCGGTACTATTTCAAAGGGTTCATGCAAAAAGCATGAGAGGGTTA	5410
Db	241	GAGGCGAAATTGTGCCCGTTTGTTCCTAAAGGGTTCCTTGCAAGACATGTGTGAATGA	3000
Qy	542	GTTTCAGTGTGATGGAGAGACTACTTTGAGCTAGTATTTGATCAGCAATGTGGGGGTG	6010
Db	301	GGTTACATCATATGGAAGAGACTATTTGAGCTTGTATGATTAAGCAATGTTGTGGCG	3600
Qy	602	CTGATTCATCCATATCATGTGTTCAATTAAGGCTCAAAAATCTGATGATGGCAATGTCA	6610
Db	361	CAGGATCTATTCACAGTCTGTGTCATATCAAGAGGCTCCAAAATCGGGTGGATGGCAATGTCAA	4200
Qy	662	GAATTTGGGTTCTAATTGGCAATCCAAATGGATTTGAATGTCAATCTTGTCCCTCA	7210
Db	421	GGAATCGGGAGCTTAATCGGCATCAATCAATGCTATCTCAATGGCCAAATCTGTGCTCA	4800
Qy	722	GGGTTCACACACTGATGGAGAGCAAGATTTTCCAAATATTTCCAGTATGTTGA	7810
Db	481	GGGTTCACACTACTATATGTGTGATCTGCTATTTCCGACATCTGTGCTGCAAAATTGGG	5400
Qy	782	CATTGGCCAAACTTCTCTAGCCAGTTCAAGTTCT	817

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QY 248 CTTAAGCACTGCTATTATATGATGAGAGCTTCGTGCTGAGTGTACAAATATAT 307
    |||||
DB 496 CTTTAAGCACTGCTATTATATGATGAGAGCTTCGTGCTGAGTGTACAAATATAT 555
    |||||
QY 308 GTGATTACAATAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 367
    |||||
DB 556 GTGATTACAATAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 615
    |||||
QY 368 CAAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCT 427
    |||||
DB 616 CAAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCT 675
    |||||
QY 428 CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
    |||||
DB 676 CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
    |||||
QY 488 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
    |||||
DB 736 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
    |||||
QY 548 GTGTGAATGAGAGGAGCTACTTGTGAGTGTGATGATGATGATGATGATGATGATGAT 607
    |||||
DB 796 GTGTGAATGAGAGGAGCTACTTGTGAGTGTGATGATGATGATGATGATGATGATGAT 855
    |||||
QY 608 CCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
    |||||
DB 856 CCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 915
    |||||
QY 668 GGGGTTCTAATTTGGCAATCCAAATGCGTATGATGATGATGATGATGATGATGATGAT 727
    |||||
DB 916 GGGGTTCTAATTTGGCAATCCAAATGCGTATGATGATGATGATGATGATGATGATGAT 975
    |||||
QY 728 CCAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
    |||||
DB 976 CCAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
    |||||
QY 788 GCCAACTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
    |||||
DB 1036 GCCAACTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1095
    |||||
QY 848 TGAAGCGTGTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 907
    |||||
DB 1096 TGAAGCGTGTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1155
    |||||
QY 908 TATTTCCATCACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
    |||||
DB 1156 TATTTCCATCACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1215
    |||||
QY 967 ATCAACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1026
    |||||
DB 1216 ATCAACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1275
    |||||
QY 1027 TTTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1070
    |||||
DB 1276 TTTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1319
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10567
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700944591_FLI
US-10-425-114-10567

Query Match          91.9%; Score 1001.2; DB 7; Length 1134;
Best Local Similarity 99.6%; Pred. No. 4e-224;
Matches 1014; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 8 CTTCAACCTCTCATCATATGAGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 67
    |||||
DB 117 CTTCAACCTCTCATCATATGAGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 176
    |||||
QY 68 TTGTTTGGGTAGCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 127
    |||||
DB 177 TTGTTTGGGTAGCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 236
    |||||
QY 128 CTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
    |||||
DB 237 CTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296
    |||||
QY 188 TGGGGGAGAGCTGTGGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
    |||||
DB 297 TGGGGGAGAGCTGTGGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356
    |||||
QY 248 CTTAAGCACTGCTATTATATGATGAGAGCTTCGTGCTGAGTGTACAAATATATAT 307
    |||||
DB 357 CTTAAGCACTGCTATTATATGATGAGAGCTTCGTGCTGAGTGTACAAATATATAT 416
    |||||
QY 308 GTGATTACAATAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 367
    |||||
DB 417 GTGATTACAATAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
    |||||
QY 368 CAAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCA 427
    |||||
DB 477 CAAACTTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCAATTTTGGCTTCCCA 536
    |||||
QY 428 CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
    |||||
DB 537 CACTCAAGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
    |||||
QY 488 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
    |||||
DB 597 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
    |||||
QY 548 GTGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
    |||||
DB 657 GTGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
    |||||
QY 608 CCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
    |||||
DB 717 CCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
    |||||
QY 668 GGGGTTCTAATTTGGCAATCCAAATGCGTATGATGATGATGATGATGATGATGATGATGAT 727
    |||||
DB 777 GGGGTTCTAATTTGGCAATCCAAATGCGTATGATGATGATGATGATGATGATGATGATGAT 836
    |||||
QY 728 CCAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
    |||||
DB 837 CCAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
    |||||
QY 788 GCCAACTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
    |||||
DB 897 GCCAACTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 956
    |||||
QY 848 TGAAGCGTGTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 907
    |||||
DB 957 TGAAGCGTGTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1016
    |||||

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RESULT 2
US-10-425-114-10567
; Sequence 10567, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

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US-10-437-963-93722
; Sequence 93722, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 93722
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92079C.1
US-10-437-963-93722

Alignment Scores:
Pred. No.: 3,39e-104 Length: 843
Score: 920.00 Matches: 168
Percent Similarity: 73.06% Conservative: 30
Best Local Similarity: 61.99% Mismatches: 53
Query Match: 65.57% Indels: 20
DB: 7 Gaps: 3

US-10-660-499a-2 (1-255) x US-10-437-963-93722 (1-843)
QY 5 MetLeuValIleuGIySerIleuGIyLeuCySeCySphenThr----- 18
DB 25 TTGCTTTTCTCGCAGTCAACGCGCTTCGTTCTGCTGACGCGGCCGACGACTCGGCC 84
QY 19 -----1leThrThyTAlaIleSerProSerGly----- 28
DB 85 AATGACGCGGCGACGACGACGACGAGTGGCTCCGTCGTCATCGACCGACGCGGCT 144
QY 29 -----TTrpThrsnAlaHleAlaThrPheThyTGIySerAspAlaSerGIyThr 45
DB 145 CCGCCCGTGGCTGAGGCGACGCGCTTCTACGCGCGCGGACGCGCTGCGGACCT 204
QY 46 MetGIyGIyAlaCySgIyTyrGIyAsnLeuTyrAlaThrGIyTyrGIyThrArgThrAla 65
DB 205 ATGGAGGCGCGCTGCGCTTACCTTACCTGCGAGGGGTATGGAGCGCGGAACGCG 264
QY 66 AlaLeuSerThrAlaLeuPheAsnAspGIyAlaSerCySgIyGlnCyTyrIlySilelle 85
DB 265 GCGCTGAGCAGCGCGCTTCAACGACGCGCGCTGCGGACGCTGCTCAAGATCGCC 324
QY 86 CyAspTyrIlySerAspSerArgTyrPheIleIySgIyArgSerValThrValThrAla 105
DB 325 TGGACCGCGAAGGCGACCGCAGTGTGCGAGCGCGCTCAACGCTCACCATCACCGCC 384
QY 106 ThrAsnPheCySProPheAsnPheAlaLeuProAsnAsnAngIyGIyTyrCySAsnPro 125
DB 385 ACCAATCTTCTGCGCGCGCGCTGAGACCTCCCGACGACAAACGCGGCTGTGCAACCT 444
QY 126 ProLeuIyHleIlePheAspMetAlaGlnProAlaTyrPheIlySgIyTyrArgGIy 145
DB 445 CCAAGCGCGGCACTTCGATATGCGCGACCGCGCTGGAAGAAATCGGTATTTACCGTCC 504
QY 146 GLyTlleValProValIleuPheGlnArgValProCySlySlyHleSgIyGIyValArgPhe 165
DB 505 GGCATCATCCCGCTCATCTCAACAAAGGCTTCATGTAAAGAAAGGTGTGTGGGTTC 564
QY 166 SerValAsnGIyArgAspTyrPheGluLeuValIleSerAsnValGIyGIyAlaGIy 185

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DB 565 ACCATCAACGGGCGATGACTTCAATCTCGTTCTTGACCAACGCTTGCACCAACCGCC 624
QY 186 SerIleGlnSerValPheIleIySgIySer---LysThnGIyTyrMetAlaMetSerArg 204
DB 625 TTGATCAAGTGAATGATGATGATGCGCTCAACCTCAACGACTGCGCTGCAATGTGAGA 684
QY 205 AsnTyrPheSerAsnTyrPheGlnSerAsnAlaTyrTleuAsnGIyGlnSerLeuSerPheArg 224
DB 685 AACTGGGGTGCMAATTTGGCACTCGTTATCGTATCTCATGACAGATGCTTCTTTAGG 744
QY 225 ValThrThrThrAspGIyGluThrArgValPheGlnAspIleValProValSerTyrThr 244
DB 745 GTACCAACATGAGACGGCCAGACGCTTGTCTTCAAGAACATTGTGCGCTGAGATGAGA 804
QY 245 PheGIyGlnThrPheSerSerProValGlnPhe 255
DB 805 TTCGGGCAAAACATTGCAAGCAAACTGCAATTC 837

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Search completed: January 12, 2006, 00:16:04
Job time : 834 secs

DB: 7 Gaps: 2

US-10-660-499A-2 (1-255) x US-10-437-963-31386 (1-1998)

QY 4 ILeMeLeValLeuGIySerLeuIleGIyLeuCySeCySpHeThrlIerThrTyr--- 22
::: |||
Db 30 GAGCTGCTGCAGAGTCGCGCATGTCAGCGCGCGCGCGCAACGAGGAGCGAACCGCC 89
QY 23 -----AlaPheSerProSerGIYTPThrAsnAlaHisAlaThrPheTYrGIYGIY 39
::: |||
Db 90 ACAAAACCGGTGGCTCGCGCCGACCGAGTGGCAGAAAGCGCAGCGGAGGTTCTACGGCGGC 149
QY 40 SerAspAlaSerGIYThrMetGIYAlaCYSeGIYTYrGIYAsnLeuTYrAlaThnGIY 59
::: |||
Db 150 GCGAGACCGCTCGGGCACCGATGGCGGGCGCTGGGATACCGCAACCTGTACTCGCAGGG 209
QY 60 TYrGIYThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGIYAlaSerCYGIY 79
210 TACGGCACCGGAAACCGCGGCTGAGACCGCGCTGTTCACACACGCGCGCTCGCGGG 269
QY 80 GINCYeTYrIleIleIleCYeAspTYrLYeSerAspSerArgTPCYsIleYGIYArg 99
270 CAGTGTACAGATCCGCTGCAGACCGCAAGAGGGCGCGCGAGTGTCAAGACCGCGGCTC 329
QY 100 SerValThrValThrAlaThrAsnPheCYeProProAsnHeAlaLeuProAsnAsn 119
::: |||
Db 330 ACCGTTACCATCACCGCACCAATTTCTGCCCGCCACATCGGAACCTTCCAGGATPAT 389
QY 120 GIYGIYTPCYeAsnProProLeuLYeHisPheAspMetAlaGInProAlaTPRGIYLYs 139
390 GGTGGCTGGTGCACCCACCAACCGCGCGCATTTGCACATGGCACACGCGGCTGGAGAG 449
QY 140 ILeGIYTYrArgIYGIYIleValProValIleuPheGlnArgValProCYeLYs 159
::: |||
Db 450 ATCGGCGTCTACAGCCACGCGCATCATACCGGTATCATCAAGAGGTTCTTGGTGAAG 509
QY 160 HisGIYGIYValArgPheSerValAsnGIYArgAspTYrPheGlnLeuValIleuIleSer 179
::: |||
Db 510 AAGGGTGGCTGGGTTCACCATTAACGGTCACGACATCACTTCAGCTAGTACGTGAC 569
QY 180 AsnValGIYGIYAlaGIYSerIleGInSerValPheIleYGIYSerLYsThrGIY--- 198
570 AACGTGGCGCGCGCACGGGTCAATCAAGTCCATGAGAGTTTATGGTTCCACACACGCGGAT 629
QY 199 TrpMetAlaMetSerArgAsnTPRGIYSerAsnTPRGIYSerAsnAlaTYrLeuAsnGIY 218
630 TCGATCCGATGCGACGTAACTGGGGCGCCAAATGGCATCACTACGCGCTACCGGT 689
QY 219 GInSerLeuSerPheArgValThrThrThrAspGIYGIYThrArgValPheGlnAspIle 238
::: |||
Db 690 CAAAGCTCTATCCCTTTGGGGTCACCAACACAGATGACCAAAACGCTGCTTCACCAACGTC 749
QY 239 ValProValSerTPRThrPheGIYGIYThrPheSerSerProValGInPhe 255
750 GTGCCACCAAGATGGAAGTTTGGCCAGACATTTGCACAGCAAGCTGCAAGTTTC 800

RESULT 14
US-10-437-963-94781
; Sequence 94781, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukhariou, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

DB	Seq ID	Seq ID NOS	Current Filing Date	Number of Seq ID NOS	Seq ID	Length	Type	Organism	Feature	Other Information	Clone ID	Pat. No.
Db	1	1	2003-05-14	204966	1	789	DNA	Oryza sativa				
Db	2	2	2003-05-14	204966	2	789	DNA	Oryza sativa				
Db	3	3	2003-05-14	204966	3	789	DNA	Oryza sativa				
Db	4	4	2003-05-14	204966	4	789	DNA	Oryza sativa				
Db	5	5	2003-05-14	204966	5	789	DNA	Oryza sativa				
Db	6	6	2003-05-14	204966	6	789	DNA	Oryza sativa				
Db	7	7	2003-05-14	204966	7	789	DNA	Oryza sativa				
Db	8	8	2003-05-14	204966	8	789	DNA	Oryza sativa				
Db	9	9	2003-05-14	204966	9	789	DNA	Oryza sativa				
Db	10	10	2003-05-14	204966	10	789	DNA	Oryza sativa				
Db	11	11	2003-05-14	204966	11	789	DNA	Oryza sativa				
Db	12	12	2003-05-14	204966	12	789	DNA	Oryza sativa				
Db	13	13	2003-05-14	204966	13	789	DNA	Oryza sativa				
Db	14	14	2003-05-14	204966	14	789	DNA	Oryza sativa				
Db	15	15	2003-05-14	204966	15	789	DNA	Oryza sativa				
Db	16	16	2003-05-14	204966	16	789	DNA	Oryza sativa				
Db	17	17	2003-05-14	204966	17	789	DNA	Oryza sativa				
Db	18	18	2003-05-14	204966	18	789	DNA	Oryza sativa				
Db	19	19	2003-05-14	204966	19	789	DNA	Oryza sativa				
Db	20	20	2003-05-14	204966	20	789	DNA	Oryza sativa				
Db	21	21	2003-05-14	204966	21	789	DNA	Oryza sativa				
Db	22	22	2003-05-14	204966	22	789	DNA	Oryza sativa				
Db	23	23	2003-05-14	204966	23	789	DNA	Oryza sativa				
Db	24	24	2003-05-14	204966	24	789	DNA	Oryza sativa				
Db	25	25	2003-05-14	204966	25	789	DNA	Oryza sativa				
Db	26	26	2003-05-14	204966	26	789	DNA	Oryza sativa				
Db	27	27	2003-05-14	204966	27	789	DNA	Oryza sativa				
Db	28	28	2003-05-14	204966	28	789	DNA	Oryza sativa				
Db	29	29	2003-05-14	204966	29	789	DNA	Oryza sativa				
Db	30	30	2003-05-14	204966	30	789	DNA	Oryza sativa				
Db	31	31	2003-05-14	204966	31	789	DNA	Oryza sativa				
Db	32	32	2003-05-14	204966	32	789	DNA	Oryza sativa				
Db	33	33	2003-05-14	204966	33	789	DNA	Oryza sativa				
Db	34	34	2003-05-14	204966	34	789	DNA	Oryza sativa				
Db	35	35	2003-05-14	204966	35	789	DNA	Oryza sativa				
Db	36	36	2003-05-14	204966	36	789	DNA					

QY 125 ProProLeuIyEhIshpEshpMeAlaGInProAlaTrpGluIySIlleGlyIleTyArg 144
 Db 183 CCAACCCCTCAGACACTTCACATGCTCAGCTCGCTGGAGAAAGATTGGTATCTACAA 242
 QY 145 GtGlyIleValProValIleupheGlnArgValProCyElyshIshIsgIyValArg 164
 Db 243 GCGGGAATTGTGCCCTTTTGTTCACAAAGGTTCTTGGACAGAGCATGGTGGAGGAG 302
 QY 165 PheSerValAsnGlyArgAspTyPheGluLeuValIleSerAsnValGlyIleAla 184
 Db 303 TTCACGATCAATGAGAGAGACTATTCGAGCTGTATGATGACATGTGTGCGCGCA 362
 QY 185 GlySerIleGlnSerValPheIleIySgIySerTyThGlyTrpMetIleMetSerArg 204
 Db 363 GGAATCATCAGCTGTGTCTTCACCAAGGCTCCAAAACGCGGTGAGATGGCAATGTCAAG 422
 QY 205 AsnTrpGlySerAsnTrpGlnSerAsnAlaTyPLeuAsnGlyGlnSerLeuSerPheArg 224
 Db 423 AACTGGAGAGCTACTCGGCATCCATGCTATCTCATAGGCCAATCATTTGTCTCAAG 482
 QY 225 ValThrThrThrAspGlyGluThrArgValPheGlnAspIleValProValSerTrpThr 244
 Db 483 GTACACACTACTGATGGTGTGACTCGTCTATTTCTGACATCGTGCCTGCAATGGGGT 542
 QY 245 PheGlyGlnThrPheSerSerProValGlnPhe 255
 Db 543 TTGGCCAGACTTCTCTAGCAAACTACATTC 575

RESULT 12

US-10-437-963-33939
 / Sequence 33939, Application US/10437963
 / Publication No. US20040123343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 33939
 / LENGTH: 1046
 / TYPE: DNA
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_38002C.1
 US-10-437-963-33939

Alignment Scores:

Pred. No.: 4.01e-106 Length: 1046
 Score: 936.50 Matches: 165
 Percent Similarity: 83.33% Conservative: 35
 Best Local Similarity: 68.75% Mismatches: 33
 Query Match: 66.75% Indels: 7
 DB: 7 Gaps: 2

US-10-660-499A-2 (1-255) x US-10-437-963-33939 (1-1046)

QY 16 CyEphethrIleThrThrTyAlaPheSerProSerGlyTrpThrAsnAlaIshAlaThr 35
 Db 109 TGCATGCGCGGACGCGCGCGCGCTCAGTGGCAGC-----GCCACG 150
 QY 36 PheTyGlyGlySerAspAlaSerGlyThrMetGlyGlyAlaCySgIyTyTrpGlyAsnLeu 55
 Db 151 TTCTACGCGCGGAGCGAGCGCTCCGGCACAATGGCGCGCGGTGCGGTACGGCAACTG 210

QY 56 TyAlaThrGlyTyTrGlyThrArgThrAlaAlaSerThrAlaLeuPheAsnAspGly 75
 Db 211 TACTGAGCGGGGTACGGAGCGAACAAGCGGCGCTGAGCTCGGCTGTTCACACGACGCG 270
 QY 76 AlaSerCySgIyGlnCySerTyIleIleIyCyAspTyTyIySerAspSerArgTrpCyS 95
 Db 271 GCGGCGTGGCGGAGGTGCTACCAAGTCACTGCGAGC---CACTGCCAATCGAAGGTGTGC 327
 QY 96 IleIySgIyArgSerValThrValThrAlaThrAsnPheCyProProAsnPheAlaLeu 115
 Db 328 AAGCGGGGACGTGGTGCATTCACCGGACCAACTCTGCGCACCGGACTTACTCAAG 387
 QY 116 ProAsnAsnAsnGlyGlyTyTrpCyAsnProProLeuIyEhIshpEshpMeAlaGInPro 135
 Db 388 CCGAGCACGAGCGCGCGCTGTCACACCGCGCGCCACGACATTGACATGGCGCAACC 447
 QY 136 AlaTrpGluIyIleGlyIleTyArgGlyGlyIleValProValIleupheGlnArgVal 155
 Db 448 GCTGGGAACAAGTGGCGCTTACCGCGCGGCGATGTCCCGTCAATTTCAGAGGGTG 507
 QY 156 ProCySgIyEhIshIsgIyValArgPheSerValAsnGlyArgAspTyPheGluLeu 175
 Db 508 TCGTGACGAGGAAGAAGAGGGGTGAGGTTCAACATCAACGGGAACGCTTACTCGAGTGC 567
 QY 176 ValIleuIleSerAsnValGlyIyAlaGlySerIleGlnSerValPheIleIySgIySer 195
 Db 568 GTGCTGATACCAACTGGGCGGCGCGGCGGTGATCAATCGGTGCAATCAAGGAGACA 627
 QY 196 TyThrGlyTrpMetAlaMetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaTy 215
 Db 628 AAGACGGGGTGGGTGACATGTCTCCGAACTGGGGGCCAATCGGCAACCAACTAC 687
 QY 216 LeuAsnGlyIleSerLeuSerPheArgValIThrThrAspGlyGluThrArgValPhe 235
 Db 688 CTCACCAACCAAGGCCATCTCTTCGTGCACCTCCACCGCGGCAAGACGCTCGCTTC 747
 QY 236 GlnAspIleValProValSerTrpThrPheGlyGlnThrPheSerSerProValGlnPhe 255
 Db 748 GAGGACGTGCGCGCTGCCAATGGCAGTTCCGGCCAGACATTCACCAAGCGCGGTGAGTTC 807

RESULT 13

US-10-437-963-31386
 / Sequence 31386, Application US/10437963
 / Publication No. US20040123343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 31386
 / LENGTH: 1998
 / TYPE: DNA
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_35699C.1
 US-10-437-963-31386

Alignment Scores:

Pred. No.: 9.9e-105 Length: 1998
 Score: 928.50 Matches: 165
 Percent Similarity: 77.04% Conservative: 33
 Best Local Similarity: 64.20% Mismatches: 54
 Query Match: 66.18% Indels: 5

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 76499
LENGTH: 940
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_76488C.1
US-10-437-963-76499

Alignment Scores:
Pred. No.: 1,73e-112 Length: 940
Score: 987.00 Matches: 174
Percent Similarity: 83.61% Conservative: 30
Best Local Similarity: 71.31% Mismatches: 38
Query Match: 70.35% Indels: 2
DB: 7 Gaps: 1

US-10-660-499a-2 (1-255) x US-10-437-963-76499 (1-940)

14 LeuCyGcSphethrllethrtThyralaPheSerProserglYTrpThraAnaLahis 33
55 CTCGCCGCCGCTCGACGACGGTGAAGGCGTCCGCGCTCGAGACCAAGGCGACC 114
34 AlathPheThyrlYglYsSerAaPaLaserglYThmetcYglYalaCySglYTrglY 53
115 GCCACTTCTACGCGCGGCGACGCGCTCGGACCAATGGCGGTGCGGTACCGG 174
54 AenleuTyraLathrglYTrglYThraGThraAlaLeuSerThraAlaLeuPhean 73
175 AACCTGTACACGCAAGGGTACGGAGCGCGGCGCTGAGCAGCGCGCTGTTCGAC 224
74 AaPglYAlaSerCySglYglnCySgYTrYslellelCyAspYrlySserAaPaLaserg 93
235 GACGGCGCGCTCGTGGCGGCGGTCTACGCGCTGACCTGCGACCGAGGCGGACCGCGG 294
94 TrpCyB1lelYsglYArSgSerValThraValThraAlaThraAnPheCySProPheanPhe 113
295 TGGTGGCGCGCGGGGGCGGTGATGACGATACCGGACCACTTCTGCGCGCCCACTAC 354
114 AlaLeuProAnaAnaAnnglYglYTrpCyAsnProProleuYshlPheAspMetAla 133
355 GCGCTCCCGACGACGACGCGCGCTGATGACCGCGCGGCGGCGACCTTCGACATGGCG 414
134 GlnProAlaTrpGluYslelYglYleYTrgYsYglYleValProValLeuPheGln 153
415 CAGCCCGCGTGGAGCGGATCGCGGTGTACCGGGGCGGCACTGTGCGGGGTGCGTCCGC 474
154 ArgValProCySglYsYshlYsYglYValArgPheSerValAnnglYArSgPhe 173
475 CGGTGGCGCGGAGCGCGCGGGCGGTGATGACCGGTGACCGGCGGCGGACTACTTC 534
174 GluLeuValLeuLeuSerAaPaLaserglYalaYslelYslelYslelYslelYs 193
535 GACCTGCTGTGATGACGAAGTGGCGCGGTGATGATGATGATGATGATGATGATGATG 594
194 GlySerYs-----ThrglYTrpMetAlaMetSerArgAnTrpGlySerAnTrpGln 211
595 GCGAGCGCGCGGTGGCGCGCGGTGATGATGATGATGATGATGATGATGATGATGATG 654

212 SerAnaLAtYrleuAnaGlYlnSerleuSerPheArgValThrThraPglYglu 231
655 TCGGTGGGTACTCTGACGCGGCGGCGCTCTGCTCCGGGTACCGGACCGACCGGCGAG 714
232 ThraGValPheGlnAsp1leValProValSerTrpThraPheGlyGlnThraPheSer 251
715 ACCATGCTCTGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 774
252 ProValGlnPhe 255
775 ACCGACGACTTC 786

RESULT 9

US-10-437-963-29573

Sequence 29573, Application US/10437963

Publication No. US2004012343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 29573

LENGTH: 1204

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_34061C.1

US-10-437-963-29573

Alignment Scores:

Pred. No.: 2.1e-110 Length: 1204
Score: 971.50 Matches: 168
Percent Similarity: 84.62% Conservative: 30
Best Local Similarity: 71.79% Mismatches: 35
Query Match: 69.24% Indels: 1
DB: 7 Gaps: 1

US-10-660-499a-2 (1-255) x US-10-437-963-29573 (1-1204)

23 AlaPheSerProserglYTrpThraAnaLahisAlaThrPheTrglYglYsSerAaPaLa 42
188 GCGCTGACCGCGGCGGTGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
43 SerGlyThmetcYglYalaCySglYTrglYAnleuTyraLathrglYTrglYTr 62
248 TCGGAACCATGGCGGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 307
63 ArgThraAlaLeuSerThraAlaLeuPheAnaAspGlyAlaSerCySglYglnCySgYr 82
308 AGGACGCGCGGCTCGACGACGCGGCTGTTCACGAGCGGCTCGCGCGGCGGTCTAC 367
83 LyslellelCyAspYrlySserAaPaLaserglYTrpCyB1lelYsYglYArSgSerVal 102
368 AGCTGCTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
103 ValThraAlaThraAnPheCySProPheanPheAlaLeuProAnaAnaAnnglYglY 122
428 ATCAGCGGCGGCACTTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
123 CyAsnProProleuYshlPheAspMetAlaGlnProAlaTrpGluYslelYslelY 142
488 TGCACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 547

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QY      8 LeuGlySerLeuIleGlyLeuCySPheThrIleThrThyAlaPheSerProSer 27
      116 CTTGCGTTCCTCTTGGCGGCGCTTCTCTGAGAGAACCCGTCGCTCTCGGGGCTC 175
QY      28 GlyTrpThrAsnAlaHisAlaThrPheTyrglyGlySerAspAlaSerGlyThrMetGly 47
      176 GGGCTAAACAAAGCGCTTCCGACCTTCTATGCGGTAGCGACCTTCAGAACGATGGGT 235
QY      48 GlyAlaCyseGlyTyrglyAsnLeuTyraIaThrGlyTyrglyThrArgThrAlaAlaLeu 67
      236 GGGCGCTGTGGGTAGACGGCAACCTGTACTCGACGGGGTAGCGGACGGACCGGGGGCTG 235
QY      68 SerThrAlaLeuPheAsnAspGlyAlaSerCyseGlyGlnCyseTyrglyIleIleCyseAsp 87
      296 AGCAGCGCGCTCTTCAACGACGCGCGCTCGTGGCGGAGTGTACCGGATCCCTCGACG 355
QY      88 TyrIySerAspSerArgTrpCyseIleGlyAlaArgSerValThrValThrAlaThrAsn 107
      356 TACAAAGCGGACCGCGGCTTCTGATCCGCGGACCGGTGACATCAACCGCCACCAAC 415
QY      108 PheCyProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrglyAsnProProLeu 127
      416 CTGTGCTCTCCCACTACGCGCTGTGCCAAGACGACGCGCGCTGTGTCAACCCGCGCG 475
QY      128 LysHisPheAspMetAlaGlnProAlaIaTrpGlyLysIleGlyIleTyraArgIlyGlyIle 147
      476 CAGCACTTCGACATGCGCGGACCGCGCTGTGCTCAAGATCGGACATCAACCGCGCGC 535
QY      148 ValProValLeuPheGlnArgValProCyseLysLysHisGlyGlyValaArgPheSerVal 167
      536 GTGCCCGTCAACCAACAAAGGTGCGGTGTGTGAAGAAACCGGGGTGAGTTCACAC 595
QY      168 AsnGlyArgAspTyrglyPheGlyLeuValLeuIleSerAsnValGlyGlyAlaGlySerIle 187
      596 AACGGCGCGGACACTTCCAGCTGTGTCTCATCTTCAACCTGGCGCGCTCGGGTCCATC 655
QY      188 GlnSerValPheIleLysGlySerLysTyrglyTyrglyMetAlaMetSerArgAsnTrpGly 207
      656 CAGTCGCGCTCCATCAAGGGGGTGTGCGCACCGGGGTGATGGCCATGTCCCGGAATGG 715
QY      208 SerAsnTrpGlnSerAsnAlaTyrlaLeuAsnGlyGlnSerLeuSerPheArgValIaThr 227
      716 GTCAACTGTGACGTCAACGCGTACCTCAAGGCGCAAGCGCTGTCCAGGTCAACGAC 775
QY      228 ThrAspGlyGlyIaThrArgValPheGlnAspIleValProValSerTrpThrPheGlyGln 247
      776 AGGAGCGGCGACGACAAACCTTCCCGGACGTGCGGCCCGCCAGCTGGGGGTTCGGTCA 835
QY      248 ThrPheSerSerProValGlnPhe 255
      836 ACGTTTGGACACTCGGACGAGGTTTC 859
      Db
      RESULT 7
      US-10-437-963-100529
      ; Sequence 100529, Application US/10437963
      ; Publication No. US20040123343A1
      ; GENERAL INFORMATION:
      ; APPLICANT: La Rosa, Thomas J.
      ; APPLICANT: Kovalic, David K.
      ; APPLICANT: Zhou, Yihua
      ; APPLICANT: Cao, Yongwei
      ; APPLICANT: Wu, Wei
      ; APPLICANT: Boukharov, Andrey A.
      ; APPLICANT: Barbasuk, Brad
      ; APPLICANT: Li, Ping
      ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
      ; FILE REFERENCE: 38-21(53221)B
      ; CURRENT APPLICATION NUMBER: US/10/437,963
      ; CURRENT FILING DATE: 2003-05-14
      ; NUMBER OF SEQ ID NOS: 204966
      ; SEQ ID NO 100529
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      ; LENGTH: 1187
      ; TYPE: DNA
      ; ORGANISM: Oryza sativa
      ; FEATURE:
      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_98236C.1
      US-10-437-963-100529
      Alignment Scores:
      Pred. No.: 7, 82e-119
      Score: 1039.00
      Percent Similarity: 85.37%
      Best Local Similarity: 73.17%
      Query Match: 74.06%
      DB: 7
      Gaps: 0
      US-10-660-499a-2 (1-255) x US-10-437-963-100529 (1-1187)
QY      10 SerLeuIleGlyLeuCysePheThrIleThrThyAlaPheSerProSerGlyTyrgly 29
      69 GCATGTGCGGACGATGCTCTCTTGAACGAGCCGCAATCGTCAAGCGCTCGGCTGG 128
QY      30 ThrAsnAlaHisAlaThrPheTyrglyGlySerAspAlaSerGlyThrMetGlyGlyAla 49
      129 AACAAAGCGTTCGCCACTTCTTACGCGGCGGACGTACGCTTCAAGAACATGGGTGGGG 188
QY      50 CyseGlyTyrglyAsnLeuTyraIaThrGlyTyrglyThrArgThrAlaAlaLeuSerThr 69
      189 TGTGGGTACGGGAGACTGTACTCGACGCGGGTACGGGACCAACGCGCGCTGAGCACG 248
QY      70 AlaLeuPheAsnAspGlyAlaSerCyseGlyGlnCyseTyrglyLysIleIleCyseAspTyrgly 89
      249 GTGCTGTCAACGACCGGGCGTGTGTGGGAGTGTACCGGATGTGCGACTACAC 308
QY      90 SerAspSerArgTrpCyseIleLysGlyArgSerValThrValThrAlaThrAsnPheCyse 109
      309 GCGGACAGCGGCTTCTGATCTCCGCAAGTGGTACATCAACGCGGACCAACCTCTCC 368
QY      110 ProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrglyCyseAsnProProLeuLysHis 129
      369 CCGCGCAATCAAGCGCTGCCCAACGACGCGCGGTGTGTCAACCCGCGCGGACGAC 428
QY      130 PheAspMetAlaGlnProAlaIaTrpGlyLysIleTyrglyArgGlyGlyIleValPro 149
      429 TTGCAATGTGCGGACCGCGGTGTGCTCAAGATCGGGTGTACGTGCGGCGCATGTGCGG 488
QY      150 ValLeuPheGlnArgValProCyseLysLysHisGlyGlyValaArgPheSerValaAsnGly 169
      489 GTGATGTACAGCGGGTGTGCGGCGGACGAGCGGGGTGAGGTTCACATCAACGCG 548
QY      170 ArgAspTyrglyPheGlyLeuValLeuIleSerAsnValGlyGlyAlaGlySerIleGlnSer 189
      549 AGGAGTACTTTCGAGCTGTGTGCTCGTCCCAAGTGGGGGTGCGGTCCATCCAGTGC 608
QY      190 ValPheIleLysGlySerLysTyrglyTyrglyMetAlaMetSerArgAsnTrpGlySerAsn 209
      609 GTGTCAATCAAGGGGTGTGCGGACCGGCTGTGATGCGCATGTCCAGGAATGGGGCGTCAAC 668
QY      210 TrpGlnSerAsnAlaTyrlaLeuAsnGlyGlnSerLeuSerPheArgValIaThrThrAsp 229
      669 TGGAGTCCAAAGCTTACTTCAAGCGGACGAGCTGTCTTCAAGGTCAACGACGACGAC 728
QY      230 GlyIaThrArgValPheGlnAspIleValProValSerTrpThrPheGlyGlnThrPhe 249
      729 GGCAGAGCGTCAACCTTCTCGACGTCGCGCGGGGTGTGAGCGTTCGCGGACGACCTTC 788
QY      250 SerSerProValGlnPhe 255
      789 TCGACTTCACAGCAGTTC 806
      Db
      RESULT 8
      US-10-437-963-76499
      ; Sequence 76499, Application US/10437963
      ; Publication No. US20040123343A1
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DB 459 CAGCACTTCGACATGGCCGAGCGGCTGCTCAAGATCGGCATCCGCGCGGCATC 518
      |||
QY 148 ValProValLeuPheGlnArgValProCysLysValHISGlyGlyValArgPheSerVal 167
      |||
DB 519 GTGCCCGTAACTACCAAGGCGGCTGTGTGAAGAAAGCGGGGTGAAGTTCAACATC 578
      |||
QY 168 AaAGLYArgAspTyrPheGlnLeuValLeuIleSerAsnValGlyValAaGlySerIle 187
      |||
DB 579 AACGGGCGGACCTACTTCCAGCTGCTGCTCATCTCCAGCTGGCGCGGCTGGCTCATC 638
      |||
QY 188 GlnSerValPheIleLysGlySerLysThrGlyTyrMetAlaMetSerArgAsnTyrGly 207
      |||
DB 639 CAGTCGGCTGCATCAAGGGGCTGCGCACCGGGGTGATGGCCATGTCCCGAACTGGGGC 698
      |||
QY 208 SerAsnTyrGlnSerAsnAlaTyrLeuAaGlyGlnSerLeuSerPheArgValThrThr 227
      |||
DB 699 GTCAACTGGCAGTCCCAAGCGGTACCTCAATGGCCAGACCTGTGCTCCAGTCAACAC 758
      |||
QY 228 ThrAspGlyGluThrArgValPheGlnAspIleValProValSerTyrThrPheGlyGln 247
      |||
DB 759 AGCGACGGCCAGACCAAAACCTTCCCGACGTGCGCGCCGCGGCTGGGGTTCCGATCAG 818
      |||
QY 248 ThrPheSerSerProValGlnPhe 255
      |||
DB 819 ACGTTTGCACCTCGCAGCAGATTCC 842
      |||
RESULT 5
US-10-425-115-170810
; Sequence 170810, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 170810
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87357C.1
US-10-425-115-170810

Alignment Scores:
Pred. No.: 2,336-119 Length: 1135
Score: 1043.00 Matches: 186
Percent Similarity: 84.68% Conservative: 24
Best Local Similarity: 75.00% Mismatches: 38
Query Match: 74.34% Indels: 0
DB: 8 Gaps: 0

US-10-660-499a-2 (1-255) x US-10-425-115-170810 (1-1135)
QY 8 LeuGlySerLeuIleGlyLeuCysPheThrIleThrThrValAlaPheSerProSer 27
      |||
DB 103 CTTCGCTGCTCTGGCGGCGGCTGCTCTCTGAGAGAACCCGCGCTCTCGGCGCTCC 162
      |||
QY 28 GlyTyrThrAsnAlaHisAlaThrPheTyrGlyGlySerAspAlaSerGlyThrMetGly 47
      |||
DB 163 GGGCTAAACAAAGCGTTCGCCACCTTCTATGGCGGTAGCAGCCTTCAGAGAACATGGGT 222
      |||
QY 48 GlyAlaCysGlyTyrGlyValLeuTyrAlaThrGlyTyrGlyThrArgThrAlaAlaLeu 67
      |||
DB 223 GGGGCTTGTTGGGTACCGCAACTGTACTCGACGGGGGTACCGCAGCAGCAGCGCGGCGCTG 282
      |||
QY 68 SerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGlnCysTyrLysIleIleCysAsp 87
      |||
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DB 283 AGCAGCGGCGCTTTCAACACAGCGCGCTGTCGGGCAATGTCTACCGGATCTCTCGAC 342
      |||
QY 88 TyrLysSerAspSerAspTyrCysIleLysGlyArgSerValThrValThrAlaThrAsn 107
      |||
DB 343 TACAGCGGACCCCGGCTTCTGATCCCGGACAGTCCGTACATCAACCGCACCAAC 402
      |||
QY 108 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyTyrTyrAsnProProLeu 127
      |||
DB 403 CTGTGCGCTCCCACTAGCAGCGCTGCCCAACGACAGCAGCGGGCTGGTGAACCCGCGCG 462
      |||
QY 128 LysHisPheAspMetAlaGlnProAlaTyrGlyLysIleGlyTyrLysThrArgGlyIle 147
      |||
DB 463 CAGCACTTCGACATGGCCAGCGCGCTGTGCTCAAGATGGGATCTACCGCGCGCATC 522
      |||
QY 148 ValProValLeuPheGlnArgValProCysLysValHISGlyGlyValArgPheSerVal 167
      |||
DB 523 GTGCCCGTAACTACCAAGGCGGCTGTGTGAAGAAAGCGGGGTGAAGTTCAACATC 582
      |||
QY 168 AaAGLYArgAspTyrPheGlnLeuValLeuIleSerAsnValGlyValAaGlySerIle 187
      |||
DB 583 AACGGGCGGACCTACTTCCAGCTGCTGCTCATCTCCAGTGGCGCGGCTGGCGGTCCATC 642
      |||
QY 188 GlnSerValPheIleLysGlySerLysThrGlyTyrMetAlaMetSerArgAsnTyrGly 207
      |||
DB 643 CAGTCGGCTGCATCAAGGGGCTGCGCACCGGGGTGATGGCCATGTCCCGAACTGGGGC 702
      |||
QY 208 SerAsnTyrGlnSerAsnAlaTyrLeuAaGlyGlnSerLeuSerPheArgValThrThr 227
      |||
DB 703 GTCAACTGGCAGTCCCAAGCGGTACCTCAATGGCCAGACCTGTGCTCCAGTCAACAC 762
      |||
QY 228 ThrAspGlyGluThrArgValPheGlnAspIleValProValSerTyrThrPheGlyGln 247
      |||
DB 763 AGCGACGGCCAGACCAAAACCTTCCCGACGTGCGCGCCGCGGCTGGGGTTCCGATCAG 822
      |||
QY 248 ThrPheSerSerProValGlnPhe 255
      |||
DB 823 ACGTTTGCACCTCGCAGCAGATTCC 846
      |||
RESULT 6
US-10-425-114-28800
; Sequence 28800, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 28800
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4764-020-G11_FLI
US-10-425-114-28800

Alignment Scores:
Pred. No.: 2,796-119 Length: 1053
Score: 1042.00 Matches: 186
Percent Similarity: 84.68% Conservative: 24
Best Local Similarity: 75.00% Mismatches: 38
Query Match: 74.27% Indels: 0
DB: 7 Gaps: 0

US-10-660-499a-2 (1-255) x US-10-425-114-28800 (1-1053)
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DB:              7              Gaps:              0
US-10-660-499A-2 (1-255) x US-10-425-114-10567 (1-1134)
QY      1 MetGlyValIleMetLeuValLeuGlySerLeuIleGlyLeuCyGcysPheThrIleThr 20
DB      161 ATGGGCAAAATCATGCTTGTGGGTAGGCTTGAATGATGATGCTTCAAAATCACT 220
QY      21 ThrTyrAlaPheSerProSerGlyTyrTrpAsnAlaHisAlaThrPheTyrGlySer 40
DB      221 ACCTAGCCTTCTCAGCTTGTGATGACCAATGCCATGCCCTTTATGGGGTAGT 280
QY      41 AspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyr 60
DB      281 GATGCTTCAGAACTATGGGGGAGCTTGGGTATGGAAATCGTATGCAATGGGTAT 340
QY      61 GlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGln 80
DB      341 GGAACTAGAACTCAGCTTTAGCAGCTGCTTATTTATGATGAGAGCTTCTGTGGTCAG 400
QY      81 CysTyrLysIleIleCysAspTyrLysSerAspSerArgTyrCysIleLysGlyArgSer 100
DB      401 TGGTACAAATTTATGATGATTCAAATCAGACTTCAAGATGTCATCAAAAGAAATCT 460
QY      101 ValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAngly 120
DB      461 GTAAACGTAATCTCACAACAACTTTGCTCCCAATTCGCCCTTCTTAACAAATGGA 520
QY      121 GlyTyrCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaTrpGlyLysIle 140
DB      521 GGTGTGGTGAACCACTCAACAGATTTGATATGGCCCAACCGCTTGGAAAAGATT 580
QY      141 GlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysLysLysHis 160
DB      581 GGATATTACAGAGAGGAGATCGTCCCGTCTATTCAAGGGTTCATCAAAAAGCAT 640
QY      161 GlyGlyValAlaArgPheSerValaAnglyArgAspTyrPheGluLeuValLeuIleSerAsn 180
DB      641 GGAGGGGTAGGTTCAGTGTGAATGGAGGAGACTTATGACTGATTTGATTCAGCAAT 700
QY      181 ValGlyValAlaGlySerIleGlnSerValPheIleGlySerLysThrGlyTyrMet 200
DB      701 GTGGGGGGTCTGATTCATCAATCAGTGTTCATTAAGGCTCAAAAACCTGAGTGGATG 760
QY      201 AlaMetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaTyrLeuAsnGlyGlnSer 220
DB      761 GCATGTCAAGAAATTTGGGTTCTAATTTGCCAATCCAAATCGTATTTGATGTCATCT 820
QY      221 LeuSerPheArgValAlaThrThrAspGlyGlnThrArgValPheGlnAspIleValPro 240
DB      821 TTGTCTTCAAGGGTCAACCACTGATGAGAGCAAGAGTTTCCAAAGATATTGTTCCA 880
QY      241 ValSerTrpThrPheGlyGlnThrPheSerSerProValGlnPhe 255
DB      881 GCAAGTTGACATTCGGCCAAACTTTCTCTAGCCCAAGTTCAAGTTC 925

RESULT 2
US-10-424-599-48351
; Sequence 48351, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 48351
; LENGTH: 1510

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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1510)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14667C.1
US-10-424-599-48351

Alignment Scores:
Pred. No.:      1,35e-163      Length:      1510
Score:          1399.00      Matches:      234
Percent Similarity: 99.61%      Conservative: 0
Best Local Similarity: 99.61%      Mismatches: 1
Query Match:     7          Indels:      0
DB:              7          Gaps:        0

US-10-660-499A-2 (1-255) x US-10-424-599-48351 (1-1510)
QY      1 MetGlyValIleMetLeuValLeuGlySerLeuIleGlyLeuCyGcysPheThrIleThr 20
DB      300 ATGGGCAAAATCATGCTTGTGGGTAGGCTTGAATGATGATGCTTCAAAATCACT 359
QY      21 ThrTyrAlaPheSerProSerGlyTyrTrpAsnAlaHisAlaThrPheTyrGlySer 40
DB      360 ACTTAGCCTTCTCAGCTTGTGATGACCAATGCCATGCCCTTTATGGGGTAGT 419
QY      41 AspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrAlaThrGlyTyr 60
DB      420 GATGCTTCAGAACTATGGGGGAGCTTGGGTATGGAAATCGTATGCAATGGGTAT 479
QY      61 GlyThrArgThrAlaAlaLeuSerThrAlaLeuPheAsnAspGlyAlaSerCysGlyGln 80
DB      480 GGAACTAGAACTCAGCTTTAGCAGCTGCTTATTTATGATGAGAGCTTCTGTGGTCAG 539
QY      81 CysTyrLysIleIleCysAspTyrLysSerAspSerArgTyrCysIleLysGlyArgSer 100
DB      540 TGGTACAAATTTATGATGATTCAAATCAGACTTCAAGATGTCATCAAAAGAAATCT 599
QY      101 ValThrValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAngly 120
DB      600 GTAACCGTATCTGCCAACAATTTTGCCTCCCAATTTGGCCCTTCTTAACAAATGGA 659
QY      121 GlyTyrCysAsnProProLeuLysHisPheAspMetAlaGlnProAlaTrpGlyLysIle 140
DB      660 GGTGTGGTGAACCACTCAACAGATTTGATATGGCCCAACCGCTTGGAAAAGATT 719
QY      141 GlyIleTyrArgGlyGlyIleValProValLeuPheGlnArgValProCysLysLysHis 160
DB      720 GGTATTTACAGAGAGGAGATCGTCCCGTCTATTCAAGGGTTCATGCAAAAAGCAT 779
QY      161 GlyGlyValAlaArgPheSerValaAnglyArgAspTyrPheGluLeuValLeuIleSerAsn 180
DB      780 GGAGGGGTAGGTTCAGTGTGAATGGAGGAGACTTATGAGCTTAGATTTGATGACGAAT 839
QY      181 ValGlyValAlaGlySerIleGlnSerValPheIleGlySerLysThrGlyTyrMet 200
DB      840 GTGGGGGGTCTGATTCATCAATCAGTGTTCATTAAGGCTCAAAAACCTGATGGATG 899
QY      201 AlaMetSerArgAsnTrpGlySerAsnTrpGlnSerAsnAlaTyrLeuAsnGlyGlnSer 220
DB      900 GCATGTCAAGAAATTTGGGTTCTAATTTGCCAATCCAAATCGTATTTGATGTCATCT 959
QY      221 LeuSerPheArgValAlaThrThrAspGlyGlnThrArgValPheGlnAspIleValPro 240
DB      960 TTGTCTTCAAGGGTCAACCACTGATGAGAGCAAGAGTTTCCAAAGATATTGTTCCA 1019
QY      241 ValSerTrpThrPheGlyGlnThrPheSerSerProValGlnPhe 255
DB      1020 GCAAGTTGACATTCGGCCAAACTTTCTCTAGCCCAAGTTCAAGTTC 1064

RESULT 3

```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2006, 21:42:08 ; Search time 828 Seconds
(without alignments)
2546.7229 Million cell updates/sec

Title: US-10-660-499A-2

Sequence: 1 MGKIMVLVLSLGLCCFTT.....QDIVPVSWTFGQTFFSPVQF 255

Scoring table: BLASTUP62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 segs, 413468905 residues

Total number of hits satisfying chosen parameters: 13587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xip
-O/cgpn2.1/USPTO.spool.p/US10660499/runat.10012006.105622.16480/app_query.fasta.1.391
-DB=Published Applications_NA_Main -QPMT=Fastap -SUFFIX=p2n.tmpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10660499 @CGN 1.1.1549 @runat.10012006.105622.16480 -NCPU=6 -ICPU=3
-NO_MAP -LARGEJOINT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main.*

1: /cgpn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgpn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgpn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgpn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgpn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgpn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgpn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgpn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgpn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgpn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1399	99.7	1134	7	US-10-425-114-10567 Sequence 10567, A
2	1399	99.7	1510	7	US-10-424-599-48351 Sequence 48351, A
3	1043	74.3	1010	7	US-10-425-114-26569 Sequence 26569, A
4	1043	74.3	1029	7	US-10-425-114-17012 Sequence 17012, A
5	1043	74.3	1135	8	US-10-425-115-170810 Sequence 170810, A
6	1042	74.3	1053	7	US-10-425-114-28800 Sequence 28800, A
7	1039	74.1	1187	7	US-10-437-963-100529 Sequence 100529, A

8	987	70.3	940	7	US-10-437-963-76499 Sequence 76499, A
9	971.5	69.2	1204	7	US-10-437-963-29573 Sequence 29573, A
10	944	67.3	576	7	US-10-021-323-1681 Sequence 1681, Ap
11	944	67.3	601	7	US-10-021-323-1684 Sequence 1684, Ap
12	936.5	66.7	1046	7	US-10-437-963-33939 Sequence 33939, A
13	928.5	66.2	1998	7	US-10-437-963-31386 Sequence 31386, A
14	920	65.6	789	7	US-10-437-963-94781 Sequence 94781, A
15	920	65.6	843	7	US-10-437-963-93722 Sequence 93722, A
16	919	65.5	765	7	US-10-167-701-14955 Sequence 14955, A
17	914.5	65.2	837	7	US-10-437-963-94782 Sequence 94782, A
18	913	65.1	1455	7	US-10-425-114-8434 Sequence 8434, Ap
19	911.5	65.0	1173	7	US-10-424-599-105712 Sequence 105712, A
20	909	64.8	1447	7	US-10-424-599-76867 Sequence 76867, A
21	906	64.6	904	7	US-10-260-238-951 Sequence 951, App
22	905	64.5	1275	7	US-10-424-599-95744 Sequence 95744, A
23	901	64.2	756	7	US-10-437-963-38542 Sequence 38542, A
24	900.5	64.2	2199	9	US-10-481-032A-666 Sequence 666, App
25	900.5	64.2	2343	7	US-10-437-963-31393 Sequence 31393, A
26	898	64.0	1276	8	US-10-739-930-1086 Sequence 1086, Ap
27	894.5	63.8	1357	7	US-10-437-963-102044 Sequence 102044, A
28	892.5	63.6	956	7	US-10-425-114-10409 Sequence 10409, A
29	892.5	63.6	1372	7	US-10-424-599-103923 Sequence 103923, A
30	890.5	63.5	753	3	US-09-938-842A-91 Sequence 91, Appl
31	890.5	63.5	753	3	US-09-938-842A-91 Sequence 91, Appl
32	889	63.4	681	3	US-09-896-301-1 Sequence 1, Appl
33	885	63.1	1302	7	US-10-425-114-8720 Sequence 8720, Ap
34	883.5	63.0	1079	8	US-10-424-599-103945 Sequence 103945, A
35	881	62.8	1389	6	US-10-425-115-93870 Sequence 93870, A
36	879	62.7	735	6	US-10-259-194A-609 Sequence 609, App
37	878	62.6	1295	7	US-10-424-599-126339 Sequence 126339, A
38	876.5	62.5	747	3	US-09-938-842A-1069 Sequence 1069, Ap
39	876.5	62.5	747	3	US-09-938-842A-1069 Sequence 1069, Ap
40	874	62.3	768	3	US-09-938-842A-1046 Sequence 1046, Ap
41	874	62.3	768	3	US-09-938-842A-1046 Sequence 1046, Ap
42	873	62.2	765	7	US-10-437-963-83328 Sequence 83328, A
43	873	62.2	1357	8	US-10-425-115-93859 Sequence 93859, A
44	865.5	61.7	759	7	US-10-437-963-91731 Sequence 91731, A
45	864.5	61.6	768	7	US-10-437-963-4774 Sequence 4774, Ap

ALIGNMENTS

RESULT 1
US-10-425-114-10567
; Sequence 10567, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10567
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700944591_FLI
; US-10-425-114-10567

Alignment Scores:
Pred. No.: 9, 02e-164
Score: 1399.00
Percent Similarity: 99.61%
Best Local Similarity: 99.61%
Query Match: 99.71%
Length: 1134
Matches: 254
Conservative: 0
Mismatch: 1
Indels: 0